SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: PAUL, PREM S.
 MENG, XIANG-JIN
 HALBUR, PATRICK G.
 MOROZOV, IGOR
 LUM, MELISSA A.
- (ii) TITLE OF INVENTION: A POLYNUCLEIC ACID ISOLATED FROM A PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), A PROTEIN ENCODED BY THE POLYNUCLEIC ACID, A VACCINE PREPARED FROM OR CONTAINING THE POLYNUCLEIC ACID OR PROTEIN,
- (iii) NUMBER OF SEQUENCES: 77
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, P.C.
 - (B) STREET: 1755 S. Jefferson Davis Highway, Suite 400
 - (C) CITY: Arlington
 - (D) STATE: Virginia
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 22202
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/131,625
 - (B) FILING DATE: 05-OCT-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lavalleye, Jean-Paul M.P.
 - (B) REGISTRATION NUMBER: 31,451
 - (C) REFERENCE/DOCKET NUMBER: 4625-021-55X CIP
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 413-3000
 - (B) TELEFAX: (703) 413-2220
 - (C) TELEX: 248855 OPAT UR

(2)	INFORMATION FOR SEQ ID NO:1:	
,	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
CGG	CCGTGTG GTTCTCGCCA AT	22
(2)	INFORMATION FOR SEQ ID NO:2:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
·	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
CCC	CATTTCC CTCTAGCGAC TG	22
(2)	INFORMATION FOR SEQ ID NO:3:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
GCC	GCGGAAC CATCAAGCAC	20

(2)	INFO	RMATION FOR SEQ ID NO:4:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:4:	
CAAC	CTTGA	CG CTATGTGAGC	20
(2)	INFO	RMATION FOR SEQ ID NO:5:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:5:	
GCG	STCTG(GA TTGACGACAG	20
(2)	INFO	RMATION FOR SEQ ID NO:6:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:6:	
GAC	rgcta(GG GCTTCTGCAC	20
(2)	INFO	RMATION FOR SEQ ID NO:7:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs	

	(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
GCC.	ATTCAGC TCACATAGCG	20
(2)	INFORMATION FOR SEQ ID NO:8:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
CTCC	GTCAAGT ATGGCCGGT	19
(2)	INFORMATION FOR SEQ ID NO:9:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
GCCA	ATTCGCC TGACTGTCA	19
(2)	INFORMATION FOR SEQ ID NO:10:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
TTG	ACGAGGA CTTCGGCTG	19
(2)	INFORMATION FOR SEQ ID NO:11:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
GCTC	CTACCTG CAATTCTGTG	20
(2)	INFORMATION FOR SEQ ID NO:12:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
GTGT	'ATAGGA CCGGCAACCG	20
(2)	INFORMATION FOR SEQ ID NO:13:	20
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2062 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown 	,
	(ii) MOLECULE TYPE: cDNA	

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

60	CGGCCTCTGA	CATCGCAACT	TTGCCTTAGG	AAGACATCAG	GCTGTCCTCC	GGCAGGCTTT
120	ATATCACTGT	ACACCCGTGT	GGCGATAGGG	AGTGCCGCAC	AAAGTCCCTC	GGCGATTCGC
180	TGCTTTCTTC	GATCTTCTCA	GCATTCCTCT	AGAATTATTT	GTTACCGATG	CACAGCCAAT
240	TTGGCAATGT	AAGGTGGTAT	AAAGGGATTT	AGATGAGTGA	TATGCTTCTG	TTGCCTTTTC
300	TCAAGGAATT	GTCCAACATG	CACCAGTTAC	GCGTCAACTT	GTGGCAGTGT	GTCAGGCATC
360	CGCCCGAGAC	CATTTCATGA	GCGGCTGCTC	TTGACCATGT	TCCTTGGTAG	TACCCAACGT
420	TTTGAATGTT	CTGTTGGCAA	TTTTGGCATT	TAGCCTGTCT	GCAACTGTTT	CATGAGGTGG
480	TTTTTGTGGT	GCAATTGCTT	GCTGTTGCTC	TTGACCGCGG	GGGGAAATGC	TAAGTATGTT
540	GGCTCAAATT	CGGGAACAGC	TCAGCGCCAA	GTTGCGCTCG	GTCTTGTTTT	GTATCGTGCC
600	CTAGCTAATA	CACAGATTGG	AGCTGAATGG	ACGCTATGTG	TTACAACTTG	TACAGCTGAT
660	ATTGTCTCTT	GTTGACTCAC	TTTTTCCTGT	TGTTTTGTCA	GGCAGTGGAG	AATTTGACTG
720	GTGTCTACCG	TCTGGTCACT	ACACAGTCGG	CATTTCCTTG	CACTACTAGC	ATGGTGCCCT
780	GCCCTGGCTG	CGCGGTCTGT	GTAGCATGTA	TATGTTCTGA	TCACGGGCGG	CTGGGTTTGT
840	TACTCATGTA	GTCCTGGCGC	AGAATTGCAT	AGGCTTGCGA	CTTCGTCATT	CGTTGATTTG
900	CGGTCGCCTG	CTATCGTTGG	AGGGCAGACT	CTGGACACTA	CAACTTTCTT	CCAGATATAC
960	CTCAAAAGAG	CCTGATCGAC	TCGAAGGTCA	AAAGTTGAGG	GAAAAGGGGC	TCATCATAGA
1020	CAATGGAGTC	TTCAGCGGAA	TAACCAGAGT	GCTACCCCTG	TGGTTCCGCG	TTGTGCTTGA
1080	TGGCGTTTTC	AAGGTGCTCT	GGCTCCACAA	ATGATAGCAC	GACTTCTGTC	GTCCTTAGAT
1140	GACTGCTAGG	AGTCGCGGCC	CCTAAAGGTG	TGATATATGC	ACGCCAGTGA	TATTACCTAC
1200	TGACATTCGT	TTCGGGTACA	TGCTTTCACC	TCCTGAATTG	CTTTTGGTCT	GCTTCTGCAC
1260	CACTCCTTTG	GCAGTAGTTG	CACTATGGGA	AGGTCGCGCT	AGTACAAATA	GCACTTTCAG
1320	GTŢTGTGCTT	TCCAGATGCC	ATTCATCACC	AAACCTGGAA	TCAGCCATAG	GGGGGTGTAC

GCTAGGCCGC	AAGTACATTC	TGGCCCCTGC	CCACCACGTT	GAAAGTGCCG	CAGGCTTTCA	1380
TCCGATTGCG	GCAAATGATA	ACCACGCATT	TGTCGTCCGG	CGTCCCGGCT	CCACTACGGT	1440
CAACGGCACA	TTGGTGCCCG	GGTTAAAAAG	CCTCGTGTTG	GGTGGCAGAA	AAGCTGTTAA	1500
ACAGGGAGTG	GTAAACCTTG	TTAAATATGC	CAAATAACAC	CGGCAAGCAG	CAGAAGAGAA	1560
AGAAGGGGGA	TGGCCAGCCA	GTCAATCAGC	TGTGCCAGAT	GCTGGGTAAG	ATCATCGCTC	1620
ACCAAAACCA	GTCCAGAGGC	AAGGGACCGG	GAAAGAAAAA	TAAGAAGAAA	AACCCGGAGA	1680
AGCCCCATTT	CCCTCTAGCG	ACTGAAGATG	ATGTCAGACA	TCACTTTACC	CCTAGTGAGC	1740
GTCAATTGTG	TCTGTCGTCA	ATCCAGACCG	CCTTTAATCA	AGGCGCTGGG	ACTTGCACCC	1800
TGTCAGATTC	AGGGAGGATA	AGTTACACTG	TGGAGTTTAG	TTTGCCTACG	CATCATACTG	1860
TGCGCCTGAT	CCGCGTCACA	GCATCACCCT	CAGCATGATG	GGCTGGCATT	CTTGAGGCAT	1920
CCCAGTGTTT	GAATTGGAAG	AATGCGTGGT	GAATGGCACT	GATTGACATT	GTGCCTCTAA	1980
GTCACCTATT	CAATTAGGGC	GACCGTGTGG	GGGTAAGATT	TAATTGGCGA	GAACCACACG	2040
GCCGAAATTA	АААААААА	AA	÷			2062

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..600
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG TTG GGG AAA TGC TTG ACC GCG GGC TGT TGC TCG CAA TTG CTT TTT

Met Leu Gly Lys Cys Leu Thr Ala Gly Cys Cys Ser Gln Leu Leu Phe

1 5 10 15

TTG Leu	TGG Trp	TGT Cys	ATC Ile 20	Val	CCG Pro	TCT Ser	TGT Cys	TTT Phe 25	GTT Val	GCG Ala	CTC Leu	GTC Val	AGC Ser 30	· Ala	AAC Asn	96	5
GGG Gly	AAC Asn	AGC Ser 35	GGC Gly	TCA Ser	AAT Asn	TTA Leu	CAG Gln 40	CTG Leu	ATT Ile	TAC Tyr	AAC Asn	TTG Leu 45		CTA Leu	TGT Cys	144	1
GAG Glu	CTG Leu 50	AAT Asn	GGC Gly	ACA Thr	GAT Asp	TGG Trp 55	CTA Leu	GCT Ala	AAT Asn	AAA Lys	TTT Phe 60	Asp	TGG Trp	GCA Ala	GTG Val	192	2
GAG Glu 65	TGT Cys	TTT Phe	GTC Val	ATT Ile	TTT Phe 70	CCT Pro	GTG Val	TTG Leu	ACT Thr	CAC His 75	Ile	GTC Val	TCT Ser	TAT Tyr	GGT Gly 80	240)
GCC Ala	CTC Leu	ACT Thr	ACT Thr	AGC Ser 85	CAT His	TTC Phe	CTT Leu	GAC Asp	ACA Thr 90	GTC Val	GGT Gly	CTG Leu	GTC Val	ACT Thr 95	Val	288	3 .
TCT Ser	ACC Thr	GCT Ala	GGG Gly 100	TTT Phe	GTT Val	CAC His	GGG Gly	CGG Arg 105	TAT Tyr	GTT Val	CTG Leu	AGT Ser	AGC Ser 110	Met	TAC Tyr	336	5
															GCG Ala	3.84	F
AAG Lys	AAT Asn 130	TGC Cys	ATG Met	TCC Ser	TGG Trp	CGC Arg 135	TAC Tyr	TCA Ser	TGT Cys	ACC Thr	AGA Arg 140	Tyr	ACC Thr	AAC Asn	TTT Phe	432	?
CTT Leu 145	CTG Leu	GAC Asp	ACT Thr	AAG Lys	GGC Gly 150	AGA Arg	CTC Leu	TAT Tyr	CGT Arg	TGG Trp 155	CGG Arg	TCG Ser	CCT Pro	GTC Val	ATC Ile 160	480)
ATA Ile	GAG Glu	AAA Lys	Arg	GGC Gly 165	Lys	GTT Val	GAG Glu	Val	GAA Glu 170	Gly	CAC His	CTG Leu	ATC Ile	GAC Asp 175	CTC Leu	528	}
													ACC Thr 190	Arg		576	;
					AGT Ser			TAG								603	}

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Leu Gly Lys Cys Leu Thr Ala Gly Cys Cys Ser Gln Leu Leu Phe 1 5 10 15

Leu Trp Cys Ile Val Pro Ser Cys Phe Val Ala Leu Val Ser Ala Asn 20 25 30

Gly Asn Ser Gly Ser Asn Leu Gln Leu Ile Tyr Asn Leu Thr Leu Cys 35 40 45

Glu Leu Asn Gly Thr Asp Trp Leu Ala Asn Lys Phe Asp Trp Ala Val 50 55 60

Glu Cys Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly
65 70 75 80

Ala Leu Thr Thr Ser His Phe Leu Asp Thr Val Gly Leu Val Thr Val 85 90 95

Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Met Tyr 100 105 110

Ala Val Cys Ala Leu Ala Ala Leu Ile Cys Phe Val Ile Arg Leu Ala 115 120 125

Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe 130 135 140

Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile 145 150 155 160

Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu 165 170 175

Lys Arg Val Val Leu Asp Gly Ser Ala Ala Thr Pro Val Thr Arg Val 180 185 190

Ser Ala Glu Gln Trp Ser Arg Pro 195 200

(2)	INFORMATION	FOR	SEQ	ID	NO:16	:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG Met	GAG Glu	TCG Ser	TCC Ser	TTA Leu 5	GAT Asp	GAC Asp	TTC Phe	TGT Cys	CAT His 10	GAT Asp	AGC Ser	ACG Thr	GCT Ala	CCA Pro 15	Gln	48
AAG Lys	GTG Val	CTC Leu	TTG Leu 20	GCG Ala	TTT Phe	TCT Ser	ATT Ile	ACC Thr 25	TAC Tyr	ACG Thr	CCA Pro	GTG Val	ATG Met 30	ATA Ile	TAT Tyr	96
GCC Ala	CTA Leu	AAG Lys 35	GTG Val	AGT Ser	CGC Arg	GGC Gly	CGA Arg 40	CTG Leu	CTA Leu	GGG Gly	CTT Leu	CTG Leu 45	CAC His	CTT Leu	TTG Leu	144
GTC Val	TTC Phe 50	CTG Leu	AAT Asn	TGT Cys	GCT Ala	TTC Phe 55	ACC Thr	TTC Phe	GGG Gly	TAC Tyr	ATG Met 60	Thr	TTC Phe	GTG Val	CAC His	192
TTT Phe 65	CAG Gln	AGT Ser	ACA Thr	AAT Asn	AAG Lys 70	GTC Val	GCG Ala	CTC Leu	ACT Thr	ATG Met 75	GGA Gly	GCA Ala	GTA Val	GTT Val	GCA Ala 80	240
CTC Leu	CTT Leu	TGG Trp	GGG Gly	GTG Val 85	TAC Tyr	TCA Ser	GCC Ala	ATA Ile	GAA Glu 90	ACC Thr	TGG Trp	AAA Lys	TTC . Phe	ATC . Ile 95	ACC Thr	288
TCC Ser	AGA Arg	TGC Cys	CGT Arg	Leu	TGC Cys	TTG Leu	CTA Leu	GGC Gly	CGC Arg	AAG Lys	TAC Tyr	ATT Ile	CTG (GCC Ala	CCT Pro	336

105

GCC Ala	CAC His	CAC His 115	GTT Val	GAA Glu	AGT Ser	GCC Ala	GCA Ala 120	GGC Gly	TTT Phe	CAT His	CCG Pro	ATT Ile 125	Ala	GCA Ala	AAT Asn
GAT Asp	AAC Asn 130	CAC His	GCA Ala	TTT Phe	GTC Val	GTC Val 135	Arg	CGT Arg	CCC Pro	GGC Gly	TCC Ser 140	Thr	ACG Thr	GTC Val	AAC Asn
GGC Gly 145	ACA Thr	TTG Leu	GTG Val	CCC Pro	GGG Gly 150	TTA Leu	AAA Lys	AGC Ser	CTC Leu	GTG Val 155	TTG Leu	GGT Gly	GGC Gly	AGA Arg	AAA Lys 160
GCT Ala	GTT Val	AAA Lys	CAG Gln	GGA Gly 165	GTG Val	GTA Val	AAC Asn	CTT Leu	GTT Val 170	AAA Lys	TAT Tyr	GCC Ala	AAA Lys		
TAA															
(2)	INF	ORMA:	rion	FOR	SEQ	ID 1	NO:1	7:							
		(i) S	(A) (B)	LEI TYI	NGTH PE: 8	: 174 amino	ERIST 4 am: o ac: linea	ino a id		S		•			
	(:	Li) N	OLEC	CULE	TYPI	: E: pi	rote	in							
	(2	ci) S	SEQUE	ENCE	DESC	CRIPT	rion:	: SE(O ID	NO:	17:				
Met 1	Glu	Ser	Ser	Leu 5	Asp	Asp	Phe	Cys	His 10	Asp	Ser	Thr	Ala	Pro 15	Gln
Lys	Val	Leu	Leu 20	Ala	Phe	Ser	Ile	Thr 25	Tyr	Thr	Pro	Val	Met 30	Ile	Tyr
Ala	Leu	Lys 35	Val	Ser	Arg	Gly	Arg 40	Leu	Leu	Gly	Leu	Leu 45	His	Leu	Leu
Val	Phe 50	Leu	Asn	Cys	Ala	Phe 55	Thr	Phe	Gly	Tyr	Met 60	Thr	Phe	Val	His
Phe	Gln	Ser	Thr	Asn	Lys	Val	Ala	Leu	Thr	Met	Gly	Ala	Val	Val	Ala

Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro

Ala	His	His 115	Val	Glu	Ser	Ala	Ala 120	Gly	Phe	His	Pro	Ile 125	Ala	Ala	Asn	
Asp	Asn 130	His	Ala	Phe	Val	Val 135	Arg	Arg	Pro	Gly	Ser 140	Thr	Thr	Val	Asn	
Gly 145	Thr	Ļeu	Val	Pro	Gly 150	Leu	Lys	Ser	Leu	Val 155	Leu	Gly	Gly	Arg	Lys 160	
Ala	Val	Lys	Gln	Gly 165	Val	Val	Asn	Leu	Val 170	Lys	Tyr	Ala	Lys			
(2)	INF	ORMA	TION	FOR	SEQ	ID 1	NO:18	3:		•						
	(i)	() () ()	A) L: B) T C) S'	CE CI ENGTI YPE: TRANI OPOLO	H: 3' nuc: DEDNI	72 ba leic ESS:	ase p acio unkr	pair: 1 1 10wn	5							
	(ii)	MO:	LECU:	LE T	YPE:	CDNA	Ą									
	(vi)	(1	A) 01 B) S'	AL SORGANI Vii TRAII NDIVI	ISM: rus V: Io	poro owa									sync	drome
	(ix)	()		E: AME/I OCATI			869									
	(xi)	SE	QUEN	CE DE	ESCRI	PTIC	ON: S	SEQ]	D NO):18:						
ATG Met 1	CCA Pro	AAT Asn	AAC Asn	ACC Thr 5	GGC Gly	AAG Lys	CAG Gln	CAG Gln	AAG Lys 10	AGA A	AAG <i>l</i> Lys	AAG (Lys	GGG (Gly	AT C Asp 15	GC Gly	48
CAG Gln	CCA Pro	GTC Val	AAT Asn 20	CAG Gln	CTG Leu	TGC Cys	CAG . Gln	ATG Met 25	CTG (Leu	GGT Z Gly	AAG <i>I</i> Lys	ATC A Ile	ATC G Ile 30	SCT C Ala	CAC His	96
CAA Gln	AAC Asn	CAG Gln 35	TCC Ser	AGA Arg	GGC Gly	AAG Lys	GGA Gly 40	CCG (Pro	GGA :	AAG 1 Lys	AAA <i>I</i> Lys	AAT A Asn 45	AAG A Lys	AAG A Lys	AAA Lys	144
AAC Asn	CCG Pro 50	GAG Glu	AAG Lys	CCC Pro	CAT His	TTC Phe 55	CCT (Pro	CTA (Leu	GCG A	ACT (Thr	GAA (Glu 60	Asp	Asp	TC A	GA Arg	192

His 65	Hls	Phe	Thr	CCT Pro	Ser 70	GAG	CGT Arg	CAA Gln	TTG Leu	TGT Cys 75	CTG Leu	TCG Ser	TCA Ser	ATC Ile	CAG Gln 80
ACC Thr	GCC Ala	TTT Phe	AAT Asn	CAA Gln 85	GGC Gly	GCT Ala	GGG Gly	ACT Thr	TGC Cys 90	ACC Thr	CTG Leu	TCA Ser	GAT Asp	TCA Ser 95	Gly
AGG Arg	ATA Ile	AGT Ser	TAC Tyr 100	ACT Thr	GTG Val	GAG Glu	TTT Phe	AGT Ser 105	TTG Leu	CCT Pro	ACG Thr	CAT His	CAT His 110	ACT Thr	GTG Val
CGC Arg	CTG Leu	ATC Ile 115	CGC Arg	GTC Val	ACA Thr	GCA Ala	TCA Ser 120	CCC Pro	TCA Ser	GCA Ala	TGA			•	
(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:1	9:				•			
		(i) :	(A) (B)) LEI) TYI	NGTH PE: 8	: 12: amin	ERIST 3 am: 5 ac: linea	ino a id		3					
	(:	ii) M	MOLE	CULE	TYPI	E: p	rote	in	•						
	(:	xi) S	SEQUI	ENCE	DESC	CRIP	rion:	: SE	Q ID	NO:	19:				
Met 1	Pro	Asn	Asn	Thr 5	Gly	Lys	Gln	Gln	Lys 10	Arg	Lys	Lys	Gly	Asp 15	Gly
Gln	Pro	Val	Asn 20	Gln	Leu	Cys	Gln	Met 25	Leu	Gly	Lys	Ile	Ile 30	Ala	His
	Pro Asn		20		•			25					30		
Gln		Gln 35	20 Ser	Arg	Gly	Lys	Gly 40	25 Pro	Gly	Lys	Lys	Asn 45	30 Lys	Lys	Lys
Gln Asn	Asn Pro	Gln 35 Glu	Ser Lys	Arg Pro	Gly His	Lys Phe 55	Gly 40 Pro	25 Pro Leu	Gly Ala	Lys Thr	Lys Glu 60	Asn 45 Asp	30 Lys Asp	Lys Val	Lys Arg
Gln Asn His 65	Asn Pro 50	Gln 35 Glu Phe	20 Ser Lys Thr	Arg Pro	Gly His Ser 70	Lys Phe 55 Glu	Gly 40 Pro	25 Pro Leu Gln	Gly Ala Leu	Lys Thr Cys 75	Lys Glu 60 Leu	Asn 45 Asp Ser	30 Lys Asp Ser	Lys Val Ile	Lys Arg Gln 80
Gln Asn His 65	Asn Pro 50 His	Gln 35 Glu Phe	20 Ser Lys Thr	Arg Pro Pro Gln 85	Gly His Ser 70 Gly	Lys Phe 55 Glu Ala	Gly 40 Pro Arg	25 Pro Leu Gln Thr	Gly Ala Leu Cys 90	Lys Thr Cys 75 Thr	Lys Glu 60 Leu Leu	Asn 45 Asp Ser	30 Lys Asp Ser	Lys Val Ile Ser 95	Lys Arg Gln 80 Gly

(2) INFORMATION FOR SEQ ID NO	20:20	:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown

 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (C) INDIVIDUAL ISOLATE: Lelystad
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..603
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG Met 1	AGA Arg	TGT Cys	TCT Ser	CAC His 5	AAA Lys	TTG Leu	GGG Gly	CGT Arg	TTC Phe 10	Leu	ACT Thr	CCG Pro	CAC His	TCT Ser 15	TGC Cys	48
TTC Phe	TGG Trp	TGG Trp	CTT Leu 20	TTT Phe	TTG Leu	CTG Leu	TGT Cys	ACC Thr 25	GGC Gly	TTG Leu	TCC Ser	TGG Trp	TCC Ser 30	TTT Phe	GCC Ala	96
GAT Asp	GGC Gly	AAC Asn 35	GGC Gly	GAC Asp	AGC Ser	TCG Ser	ACA Thr 40	TAC Tyr	CAA Gln	TAC Tyr	ATA Ile	TAT Tyr 45	AAC Asn	TTG Leu	ACG Thr	144
ATA Ile	TGC Cys 50	GAG Glu	CTG Leu	AAT Asn	GGG Gly	ACC Thr 55	GAC Asp	TGG Trp	TTG Leu	TCC Ser	AGC Ser 60	CAT His	TTT (Phe	GGT ' Gly	TGG Trp	192
GCA Ala 65	GTC Val	GAG Glu	ACC Thr	TTT Phe	GTG Val 70	CTT Leu	TAC Tyr	CCG Pro	GTT Val	GCC Ala 75	Thr	CAT His	ATC (CTC ' Leu	TCA Ser 80	240
CTG Leu	GGT Gly	TTT Phe	CTC Leu	ACA Thr 85	ACA Thr	AGC Ser	CAT His	TTT Phe	TTT Phe 90	GAC Asp	GCG Ala	CTC Leu	GGT (Gly	CTC (Leu 95	GGC Gly	288
GCT Ala	GTA Val	TCC Ser	ACT Thr 100	GCA Ala	GGA Gly	TTT Phe	GTT Val	GGC Gly 105	GGG Gly	CGG Arg	TAC Tyr	GTA (CTC ' Leu 110	rgc i Cys	AGC Ser	336

(0)																
	ACT Thr															606
												CAA Gln			ACG Thr	576
												GGC Gly			Val	528
AAC Asn 145	TTC Phe	ATT Ile	GTG Val	GAC Asp	GAC Asp 150	CGG Arg	GGG Gly	AGA Arg	GTT Val	CAT His 155	CGA Arg	TGG Trp	AAG Lys	TCT Ser	CCA Pro 160	480
GCT Ala	GCT Ala 130	AAA Lys	AAT Asn	TGC Cys	ATG Met	GCC Ala 135	TGC Cys	CGC Arg	TAT Tyr	GCC Ala	CGT Arg 140	ACC Thr	CGG Arg	TTT Phe	ACC Thr	432
GTC Val	TAC Tyr	GGC Gly 115	GCT Ala	TGT Cys	GCT Ala	TTC Phe	GCA Ala 120	GCG Ala	TTC Phe	GTA Val	TGT Cys	TTT Phe 125	GTC Val	ATC Ile	CGT Arg	384

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Arg Cys Ser His Lys Leu Gly Arg Phe Leu Thr Pro His Ser Cys

1 10 15

Phe Trp Trp Leu Phe Leu Cys Thr Gly Leu Ser Trp Ser Phe Ala 20 25 30

Asp Gly Asn Gly Asp Ser Ser Thr Tyr Gln Tyr Ile Tyr Asn Leu Thr 35 40 45

Ile Cys Glu Leu Asn Gly Thr Asp Trp Leu Ser Ser His Phe Gly Trp 50 55 60

Ala Val Glu Thr Phe Val Leu Tyr Pro Val Ala Thr His Ile Leu Ser 65 70 75 80

Leu	Gly	Phe	Leu	Thr 85	Thr	Ser	His	Phe	Phe 90	Asp	Ala	Leu	Gly	Leu 95	Gly	
Ala	Val	Ser	Thr 100	Ala	Gly	Phe	Val	Gly 105	Gly	Arg	Tyr	Val	Leu 110	Cys	Ser	
Val	Tyr	Gly 115	Ala	Cys	Ala	Phe	Ala 120	Ala	Phe	Val	Cys	Phe 125	Val	Ile	Arg	
Ala	Ala 130	Lys	Asn	Cys	Met	Ala 135	Cys	Arg	Tyr	Ala	Arg 140	Thr	Arg	Phe	Thr	
Asn 145	Phe	Ile	Val	Asp	Asp 150	Arg	Gly	Arg	Val	His 155	Arg	Trp	Lys	Ser	Pro 160	
Ile	Val	Val	Glu	Lys 165	Leu	Gly	Lys	Ala	Glu 170	Val	Asp	Gly	Asn	Leu 175	Val	
Thr	Ile	Lys	His 180	Val	Val	Leu	Glu	Gly 185	Val	Lys	Ala	Gln	Pro 190	Leu	Thr	
Arg	Thr	Ser 195	Ala	Glu	Gln	Trp	Glu 200	Ala								
(2)	INFO	ORMA!	rion	FOR	SEQ	ID 1	NO:22	2:								
	(i)	(I ((A) LE 3) TY C) ST	ENGTI (PE : (RANI	HARAC H: 16 nucl DEDNI DGY:	54 ba leic ESS:	ase p acio unkr	pairs 1	5							
	(ii)	MOI	LECUI	LE T	YPE:	CDNA	Ą								-	
	(vi)	(<u>1</u>	A) OF 3) S:	RGAN: vi: RAII		poro wa		_					_	_	/ syn	drome
	(xi)	SE(QUENC	CE DI	ESCRI	PTIC	ON: S	SEQ I	D NO):22:	:					
TGG	GCTGC	GCA T	TCTI	GAGO	GC AI	CCCA	GTGT	TTG	TTAA	GGA	AGAA	TGCG	TG G	TGAA	TGGC	A 6
CTG	ATTG	ACA T	TGT	SCCTO	CT AA	GTCA	CCTA	TTC	AATT	AGG	GCGA	CCGT	GT G	GGGG'	TAAGA	12
TTT	AATTO	GGC (GAGAZ	ACCA	CA CO	GCCC	CAAAE	TAA	AAAA	AAA	AAAA	L				16

(2)	INFORMATION	FOR	SEQ	ID	NO:23:
-----	-------------	-----	-----	----	--------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (C) INDIVIDUAL ISOLATE: Lelystad
- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG GGA GGC CTA GAC GAT TTT TGC AAC GAT CCT ATC GCC GCA CAA AAG Met Gly Gly Leu Asp Asp Phe Cys Asn Asp Pro Ile Ala Ala Gln Lys 1		_								
Leu Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Ile Met Ile Tyr Ala 30 CTT AAG GTG TCA CGC GGC CGA CTC CTG GGG CTG TTG CAC ATC CTA ATA Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile 35 40 45 TTT CTG AAC TGT TCC TTT ACA TTC GGA TAC ATG ACA TAT GTG CAT TTT Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe 50 55 60 CAA TCC ACC AAC CGT GTC GCA CTT ACC CTG GGG GCT GTT GTC GCC CTT 60 Acc Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu 65 70 75 80 CTG TGG GGT GTT TAC AGC TTC ACA GAG TCA TGG AAG TTT ATC ACT TCC Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	le Ala Ala Gln Lys	Asn Asp Pro Il	TGC AAC Cys Asr	TTT Phe	GAT Asp	GAC Asp 5	CTA Leu	GGC Gly	GGA Gly	Met
Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile 40 TTT CTG AAC TGT TCC TTT ACA TTC GGA TAC ATG ACA TAT GTG CAT TTT Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe 50 CAA TCC ACC AAC CGT GTC GCA CTT ACC CTG GGG GCT GTT GTC GCC CTT Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu 65 CTG TGG GGT GTT TAC AGC TTC ACA GAG TCA TGG AAG TTT ATC ACT TCC Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	le Met Ile Tyr Ala	Tyr Thr Pro Il	Thr Tyr	ATC Ile	AGC Ser	TTT Phe	Ala	CTA Leu	GTG Val	CTC Leu
Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe 50 CAA TCC ACC AAC CGT GTC GCA CTT ACC CTG GGG GCT GTT GTC GCC CTT Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu 65 70 75 80 CTG TGG GGT GTT TAC AGC TTC ACA GAG TCA TGG AAG TTT ATC ACT TCC Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	eu His Ile Leu Ile	IG GGG CTG TTG eu Gly Leu Le	Leu Leu	CGA Arg	GGC Gly	CGC Arg	TCA Ser	Val	AAG Lys	CTT Leu
Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu 65 70 75 80 CTG TGG GGT GTT TAC AGC TTC ACA GAG TCA TGG AAG TTT ATC ACT TCC Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	r Tyr Val His Phe	Sly Tyr Met Th	TTC GGA Phe Gly	Thr	TTT Phe	TCC Ser	TGT Cys	AAC Asn	Leu	TTT Phe
Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	a Val Val Ala Leu	hr Leu Gly Al	CTT ACC Leu Thr	GCA Ala	Val	CGT Arg	AAC Asn	ACC Thr	TCC Ser	Gln
	s Phe Ile Thr Ser	lu Ser Trp Ly	ACA GAG Thr Glu	TTC Phe	AGC Ser	Tyr	GTT Val	GGT Gly	TGG Trp	CTG Leu

336

110

AGA TGC AGA TTG TGT TGC CTT GGC CGG CGA TAC ATT CTG GCC CCT GCC

Arg Cys Arg Leu Cys Cys Leu Gly Arg Arg Tyr Ile Leu Ala Pro Ala

CAT His	CAC His	GTA Val 115	GAA Glu	AGT Ser	GCT Ala	GCA Ala	GGT Gly 120	CTC Leu	CAT His	TCA Ser	ATC Ile	TCA Ser 125	GCG Ala	TCT Ser	GGT Gl	Y	384
AAC Asn	CGA Arg 130	GCA Ala	TAC Tyr	GCT Ala	GTG Val	AGA Arg 135	AAG Lys	CCC Pro	GGA Gly	CTA Leu	ACA Thr 140	TCA Ser	GTG . Val	AAC Asn	GGC Gl	Y	432
ACT Thr 145	CTA Leu	GTA Val	CCA Pro	GGA Gly	CTT Leu 150	CGG Arg	AGC Ser	CTC Leu	GTG Val	CTG Leu 155	GGC Gly	GGC Gly	AAA Lys	CGA Arg	GCT Al 16	a	480
GTT Val	AAA Lys	CGA Arg	GGA Gly	GTG Val 165	GTT Val	AAC Asn	CTC Leu	GTC Val	AAG Lys 170	TAT Tyr	GGC Gly	CGG Arg	TAA				522

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Gly Leu Asp Asp Phe Cys Asn Asp Pro Ile Ala Ala Gln Lys Leu Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Ile Met Ile Tyr Ala 30 Tyr Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile 45 The Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe 65 Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu 80 Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser 90 Arg Cys Arg Leu Cys Cys Leu Gly Arg Arg Tyr Ile Leu Ala Pro Ala

His His Val Glu Ser Ala Ala Gly Leu His Ser Ile Ser Ala Ser Gly
115 120 125

Asn	Arg 130	Ala	Tyr	Ala	Val	Arg 135	Lys	Pro	Gly	Leu	Thr 140	Ser	Val	Asn	Gly	
Thr 145	Leu	Val	Pro	Gly	Leu 150	Arg	Ser	Leu	Val	Leu 155	Gly	Gly	Lys	Arg	Ala 160	
Val	Lys	Arg	Gly	Val 165	Val	Asn	Leu	Val	Lys 170	Tyr	Gly	Arg				•
(2)	INF	ORMA	TION	FOR	SEQ	ID I	NO:2	5:								
	(i)	() () ()	A) Li B) Ti C) Si D) To	ENGT YPE: TRAN OPOLO	H: 3; nuc: DEDNI DGY:	CTER: 87 ba leic ESS: unkr	ase p acio unko nown	pair: d	3							
	(vi)	· ()		RGAN: vi:	ISM: rus						e and	d res	spira	ıtory	, syn	drome
		(<i>1</i>		AME/I	ON:	13									·	
										0:25:	•					
ATG Met 1	GCC Ala	GGT Gly	AAA Lys	AAC Asn 5	CAG Gln	AGC Ser	CAG . Gln	AAG Lys	AAA Lys 10	AAG <i>I</i> Lys	AAA A Lys	AGT A Ser	ACA G Thr	CT C Ala 15	CCG Pro	4:
ATG Met	GGG Gly	AAT Asn	GGC Gly 20	CAG Gln	CCA Pro	GTC . Val	AAT Asn	CAA Gln 25	CTG ' Leu	TGC (Cys	CAG : Gln	ΓΤG (Leu	CTG G Leu 30	GT G Gly	CA Ala	9(
ATG Met	ATA Ile	AAG Lys 35	TCC Ser	CAG Gln	CGC Arg	CAG (Gln	CAA (Gln 40	CCT / Pro	AGG (Arg	GGA (GA (Gly	CAG (Gln 45	SCC A Ala	AA A Lys	AG Lys	144
AAA Lys	AAG Lys 50	CCT Pro	GAG Glu	AAG Lys	CCA Pro	CAT ' His 55	TTT (Phe	CCC (Pro	CTG (Leu	GCT C Ala	CT C Ala 60	GAA G	AT G Asp	AC A Asp	TC Ile	192
CGG Arg 65	CAC His	CAC His	CTC Leu	ACC Thr	CAG . Gln 70	ACT (Thr	GAA (Glu	CGC (Arg	rcc (Ser	CTC I Leu 75	GC I Cys	TG C Leu	AA T Gln	CG A Ser	TC Ile 80	24(

CAG Gln	ACG Thr	GCT Ala	TTC Phe	AAT Asn 85	CAA Gln	GGC Gly	GCA Ala	GGA Gly	ACT Thr 90	GCG Ala	TCG Ser	CTT Leu	TCA Ser	TCC Ser 95	AGC Ser	288
GGG Gly	AAG Lys	GTC Val	AGT Ser 100	TTT Phe	CAG Gln	GTT Val	GAG Glu	TTT Phe 105	Met	CTG Leu	CCG Pro	GTT Val	GCT Ala 110	CAT His	ACA Thr	336
GTG Val	CGC Arg	CTG Leu 115	ATT Ile	CGC Arg	GTG Val	ACT Thr	TCT Ser 120	ACA Thr	TCC Ser	GCC Ala	AGT Ser	CAG Gln 125	GGT Gly	GCA Ala	AGT Ser	384
TAA												٠				387
(2)	INFO	ORMAT	rion	FOR	SEQ	ID I	NO:2	6:				-				
	((i) S					ERIS'									

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Gly Lys Asn Gln Ser Gln Lys Lys Lys Ser Thr Ala Pro

Met Gly Asn Gly Gln Pro Val Asn Gln Leu Cys Gln Leu Leu Gly Ala

Met Ile Lys Ser Gln Arg Gln Gln Pro Arg Gly Gln Ala Lys Lys

Lys Lys Pro Glu Lys Pro His Phe Pro Leu Ala Ala Glu Asp Asp Ile

Arg His His Leu Thr Gln Thr Glu Arg Ser Leu Cys Leu Gln Ser Ile 65

Gln Thr Ala Phe Asn Gln Gly Ala Gly Thr Ala Ser Leu Ser Ser 85 95

Gly Lys Val Ser Phe Gln Val Glu Phe Met Leu Pro Val Ala His Thr

Val Arg Leu Ile Arg Val Thr Ser Thr Ser Ala Ser Gln Gly Ala Ser 115 120 125

(2)	INFC	RMATION FOR SEQ ID NO:27:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: porcine reproductive and respiratory syndromory virus (C) INDIVIDUAL ISOLATE: Lelystad	ne
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:27:	
TTTC	GACAG'	TC AGGTGAATGG CCGCGATTGG CGTGTGGCCT CTGAGTCACC TATTCAATTA	6
GGG	CGATC	AC ATGGGGGTCA TACTTAATCA GGCAGGAACC ATGTGACCGA AATTAAAAAA	12
AAA	AAAA		12
(2)	INFO	RMATION FOR SEQ ID NO:28:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:28:	
GGGG	ATCC	GG TATTTGGCAA TGTGTC	26
(2)	INFOR	RMATION FOR SEQ ID NO:29:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	
-	(ii)	MOLECULE TYPE: DNA (genomic)	

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GGT	GTTTTCC ACGAGAACCG CTTAAGGG	28
(2)	INFORMATION FOR SEQ ID NO:30:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GGGG	GATCCAG AGTTTCAGCG G	21
(2)	INFORMATION FOR SEQ ID NO:31:	
•	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
CAGT	TAGTCG ACACGGTCTT AAGGG	25
(2)	INFORMATION FOR SEQ ID NO:32:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
GGG.	ATCCTT GTTAAATATG CC	22

(2)	INFO	RMATION FOR SEQ ID NO:33:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:33:	
CTT	ACGCA	CC ACTTAAGGG	19
(2)	INFO	RMATION FOR SEQ ID NO:34:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:34:	
AATG	GGGC'	TT CTCCGG	16
(2)	INFO	RMATION FOR SEQ ID NO:35:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 886 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown	
	(ii)	MOLECULE TYPE: cDNA	-
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: porcine reproductive and respiratory syndrome virus (B) STRAIN: Iowa (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGAGTCGT	CCTTAGATGA	CTTCTGTCAT	GATAGCACGG	CTCCACAAAA	GGTGCTCTTG	60
GCGTTTTCTA	TTACCTACAC	GCCAGTGATG	ATATATGCCC	TAAAGGTGAG	TCGCGGCCGA	120
CTGCTAGGGC	TTCTGCACCT	TTTGGTCTTC	CTGAATTGTG	CTTTCACCTT	CGGGTACATG	180
ACATTCGTGC	ACTTTCAGAG	TACAAATAAG	GTCGCGCTCA	CTATGGGAGC	AGTAGTTGCA	240
CTCCTTTGGG	GGGTGTACTC	AGCCATAGAA	ACCTGGAAAT	TCATCACCTC	CAGATGCCGT	300
TTGTGCTTGC	TAGGCCGCAA	GTACATTCTG	GCCCCTGCCC	ACCACGTTGA	AAGTGCCGCA	360
GGCTTTCATC	CGATTGCGGC	AAATGATAAC	CACGCATTTG	TCGTCCGGCG	TCCCGGCTCC	420
ACTACGGTCA	ACGGCACATT	GGTGCCCGGG	TTAAAAAGCC	TCGTGTTGGG	TGGCAGAAAA	480
GCTGTTAAAC	AGGGAGTGGT	AAACCTTGTT	AAATATGCCA	AATAACACCG	GCAAGCAGCA	540
GAAGAGAAAG	AAGGGGGATG	GCCAGCCAGT	CAATCAGCTG	TGCCAGATGC	TGGGTAAGAT	600
CATCGCTCAC	CAAAACCAGT	CCAGAGGCAA	GGGACCGGGA	AAGAAAAATA	AGAAGAAAA	660
CCCGGAGAAG	CCCCATTTCC	CTCTAGCGAC	TGAAGATGAT	GTCAGACATC	ACTTTACCCC	720
TAGTGAGCGT	CAATTGTGTC	TGTCGTCAAT	CCAGACCGCC	TTTAATCAAG	GCGCTGGGAC	780
TTGCACCCTG	TCAGATTCAG	GGAGGATAAG	TTACACTGTG	GAGTTTAGTT	TGCCTACGCA	840
TCATACTGTG	CGCCTGATCC	GCGTCACAGC	ATCACCCTCA	GCATGA		886

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 886 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-1894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGGGGTCGT	CCTTAGATGA	CTTCTGCCAT	GATAGTACGG	CTCCACAAAA	GGTGCTTTTG	60
GCGTTTTCTA	TTACCTACAC	GCCAGTGATG	ATATATGCCC	TAAAGGTGAG	TCGCGGCCGA	120
CTGCTAGGGC	TTCTGCACCT	TTTGATCTTC	CTGAATTGTG	CTTTCACCTT	CGGGTACATG	180
ACATTCGTGC	ACTTTCAGAG	TACAAATAAG	GTCGCGCTCA	CTATGGGAGC	AGTAGTTGCA	24.0
CTCCTTTGGG	GGGTGTACTC	AGCCATAGAA	ACCTGGAAAT	TCATCACCTC	CAGATGCCGT	300
TTGTGCTTGC	TAGGCCGCAA	GTACATTCTG	GCCCCTGCCC	ACCACGTTGA	AAGTGCCGCA	360
GGCTTTCATC	CGATTGCGGC	AAATGATAAC	CACGCATTTG	TCGTCCGGCG	TCCCGGCTCC	420
ACTACGGTCA	ACGGCACATT	GGTGCCCGGG	TTGAAAAGCC	TCGTGTTGGG	TGGCAGAAAA	480
GCTGTTAAAC	AGGGAGTGGT	AAACCTTGTC	AAATATGCCA	AATAACAACG	GCAAGCAGCA	540
GAAGAGAAAG	AAGGGGGATG	GCCAGCCAGT	CAATCAGCTG	TGCCAGATGC	TGGGTAAGAT	600
CATCGCTCAG	CAAAACCAGT	CCAGAGGCAA	GGGACCGGGA	AAGAAAAACA	AGAAGAAAA	660
CCCGGAGAAG	CCCCATTTTC	CTCTAGCGAC	TGAAGATGAT	GTCAGACATC	ACTTCACCCC	720
TAGTGAGCGG	CAATTGTGTC	TGTCGTCAAT	CCAGACCGCC	TTTAATCAAG	GCGCTGGGAC	780
TTGCACCCTG	TCAGATTCAG	GGAGGATAAG	TTACACTGTG	GAGTTTAGTT	TGCCAACGCA	840
TCATACTGTG	CGCTTGATCC	GCGTCACAGC	ATCACCCTCA	GCATGA		886

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 886 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGGGGTCGT	CCTTAGATGA	CTTCTGTCAT	GACAGCACGG	CTCCACAAAA	GGTGCTTTTG	60
GCGTTTTCTA	TTACCTACAC	GCCAGTGATG	ATATATGCCC	TGAAGGTGAG	TCGCGGCCGA	120
CTGCTAGGGC	TTCTGCACCT	TTTGATCTTC	CTGAATTGTG	CTTTCACCTT	CGGGTACATG	180
ACATTCGTGC	ACTTTCAGAG	TACAAATAAG	GTCGCACTCA	CTATGGGAGC	AGTAGTTGCA	240
CTCCTTTGGG	GGGTGTACTC	AGCCATAGAA	ACCTGGAAAT	TCATCACCTC	CAGATGCCGT	300
TTGTGCTTGC	TAGGCCGCAA	GTACATTCTG	GCCCCTGCCC	ACCACGTTGA	AAGTGCCGCA	360
GGCTTTCATC	CGATTGCGGC	AAATGATAAC	CACGCATTTG	TCGTTCGGCG	TCCCGGCTCC	420
ACTACGGTCA	ACGGCACATT	GGTGCCCGGG	TTGAAAAGCC	TCGTGTTGGG	TGGCAGAAAA	480
GCTGTTAAAC	AGGGAGTGGT	AAACCTTGTC	AAATATGCCA	AATAACAACG	GTAAGCAGCA	540
GAAGAGAAAG	AAGGGGGATG	GCCAGCCAGT	CAATCAGCTG	TGCCAGATGC	TGGGCAAGAT	600
CATCGCTCAG	CAAAATCAGT	CCAGAGGCAA	GGGACCGGGA	AAGAAAAATA	AGAAGAAAAA	660
CCCGGAGAAG	CCCCATTTTC	CTCTAGCGAC	TGAAGATGAT	GTCAGACATC	ACTTTACCCC	720
TAGTGAGCGG	CAATTGTGTC	TGTCGTCAAT	CCAGACCGCC	TTTAATCAAG	GCGCTGGGAC	780
TTGCACCCTG	TCAGATTCAG	GGAGGATAAG	TTACACTGTG	GAGTTTAGTT	TGCCTACGCA	840
TCATACTGTG	CGCCTGATCC	GCGTCACAGC	ATCACCCTCA	GCATGA		886

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 886 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGGGGTCGT	CCTTAGATGA	CTTCTGTTAT	GATAGTACGG	CTCCACAAAA	GGTGCTTTTG	60
GCATTTTCTA	TTACCTACAC	GCCAGTAATG	ATATATGCCC	TAAAGGTGAG	TCGCGGCCGA	120
CTGCTAGGGC	TTCTGCACCT	TTTGATTTTC	CTGAACTGTG	CTTTCACCTT	CGGGTACATG	180
ACATTCATGC	ACTTTCAGAG	TACAAATAAG	GTCGCGCTCA	CTATGGGAGC	AGTAGTTGCA	240
CTCCTTTGGG	GGGTGTACTC	AGCCATAGAA	ACCTGGAAAT	TCATCACCTC	CAGATGCCGT	300
TTGTGCTTGC	TAGGCCGCAA	GTACATTCTG	GCCCCTGCCC	ACCACGTTGA	AAGTGCCGCA	360
GGCTTTCATC	CGATTGCGGC	AAATGATAAC	CACGCATTTG	TCGTCCGGCG	TCCCGGCTCC	420
ACTACGGTCA	ACGGCACATT	GGTGCCCGGG	TTGAAAAGCC	TCGTGTTGGG	TGGCAGAAAA	480
GCTGTTAAAC	AGGGAGTGGT	AAACCTTGTC	AAATATGCCA	AATAACAACG	GCAAGCAGCA	540
GAAGAGAAAG	AAGGGGGATG	GCCAGCCAGT	CAATCAGCTG	TGCCAGATGC	TGGGTAAGAT	600
CATCGCCCAG	CAAAACCAGT	CTAGAGGCAA	GGGACCGGGA	AAGAAAAATA	AGAAGAAAA	660
CCCGGAGAAG	CCCCATTTTC	CTCTAGCGAC	TGAAGATGAT	GTCAGACATC	ACTTTACCCC	720
TAGTGAGCGG	CAATTGTGTC	TGTCGTCAAT	CCAAACTGCC	TTTAATCAAG	GCGCTGGGAC	780
TTGCACCCTG	TCAGATTCAG	GGAGGATAAG	TTACACTGTG	GAGTTTAGTT	TGCCTACGCA	840
TCATACTGTG	CGCTTGATCC	GCGTCACAGC	ATCACCCTCA	GCATGA		886

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 886 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGGGGTCGT	CCTTAGATGA	CTTCTGCCAT	GATAGCACGG	CTCCACAAAA	GGTGCTTTTG	60
GCGTTCTCTA	TTACCTAÇAC	GCCAGTGATG	ATATATGCCC	TAAAAGTAAG	TCGCGGCCGA	120
CTGCTAGGGC	TTCTGCACCT	TTTGATCTTC	CTAAATTGTG	CTTTCACCTT	CGGGTACATG	180
ACATTCGTGC	ACTTTCAGAG	CACAAACAAG	GTCGCGCTCA	CTATGGGAGC	AGTAGTTGCA	240
CTCCTTTGGG	GGGTGTACTC	AGCCATAGAA	ACCTGGAAAT	TCATCACCTC	CAGATGCCGT	300
TTGTGCTTGC	TAGGCCGCAA	GTACATTTTG	GCCCTGCCC	ACCACGTTGA	AAGTGCCGCA	360
GGCTTTCATC	CGATAGCGGC	AAATGATAAC	CACGCATTTG	TCGTCCGGCG	TCCCGGCTCC	420
ACTACGGTTA	ACGGCACATT	GGTGCCCGGG	TTGAAAAGCC	TCGTGTTGGG	TGGCAGAAAA	480
GCTGTCAAAC	AGGGAGTGGT	AAACCTTGTT	AAATATGCCA	AATAACAACG	GCAAGCAGCA	540
GAAGAAAAAG	AAGGGGGATG	GCCAGCCAGT	CAATCAGCTG	TGCCAGATGC	TGGGTAAGAT	600
CATCGCTCAG	CAAAACCAGT	CCAGAGGCAA	GGGACCGGGA	AAGAAAAACA	AGAAGAAAA	660
CCCGGAGAAG	CCCCATTTTC	CTCTAGCGAC	TGAAGATGAT	GTCAGACATC	ACTTCACCTC	720
TGGTGAGCGG	CAATTGTGTC	TGTCGTCAAT	CCAGACAGCC	TTTAATCAAG	GCGCTGGAAC	780
TTGTACCCTG	TCAGATTCAG	GGAGGATAAG	TTACACTGTG	GAGTTTAGTT	TGCCGACGCA	840
TCATACTGTG	CGCTTGATCC	GCGTCACAGC	GTCACCCTCA	GCATGA		886

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 886 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGGGTCGT	CCCTAGACGA	CTTTTGCAAT	GATAGCACGG	CTCCACAAAA	GGTGCTTTTG	60
GCGTTTTCTA	TTACCTACAC	GCCGGTGATG	ATATATGCTC	TAAAGGTAAG	TCGCGGCCGA	120
CTGCTAGGGC	TTCTGCACCT	TTTGATTTTT	CTGAATTGTG	CTTTTACTTT	CGGGTACATG	180
ACATTCGTGC	ACTTTGAGAG	CACAAATAGG	GTCGCGCTCA	CTATGGGAGC	AGTAGTCGCA	240
CTTCTCTGGG	GGGTGTACTC	AGCCATAGAA	ACCTGGAAAT	TCATCACCTC	CAGATGCCGT	300
TTGTGCTTGC	TAGGCCGCAA	GTACATTCTG	GCCCTGCCC	ACCACGTTGA	GAGTGCCGCA	360
GGCTTTCATC	CGATTGCGGC	AAATGATAAC	CACGCATTTG	TCGTCCGGCG	TCCCGGCTCC	420
ACTACGGTTA	ACGGCACATT	GGTGCCCGGG	TTGAGAAGCC	TCGTGTTGGG	TGGCAAAAAA	480
GCTGTTAAGC	AGGGAGTGGT	AAACCTTGTT	AAATATGCCA	AATAACAACG	GCAAGCAGCA	540
GAAGAAAAAG	AAGGGGGATG	GCCAGCCAGT	CAATCAGCTC	TGCCAAATGC	TGGGTAAGAT	600
CATCGCCCAG	CAAAACCAGT	CCAGAGGTAA	GGGACCGGGA	AAGAAAATA	AGAAGAAAA	660
CCCGGAGAAG	CCCCATTTTC	CTCTAGCGAC	TGAAGATGAT	GTCAGACATC	ACTTCACCCC	720
CAGTGAGCGG	CAATTGTGTC	TGTCGTCAAT	CCAGACTGCC	TTTAATCAGG	GCGCTGGGAC	780
CTGTATCCTA	TCAGATTCAG	GGAGGATAAG	TTACACTGTG	GAGTTTAGTT	TGCCGACGCA	840
TCATACTGTG	CGCCTGATTC	GCGTCACGGC	ACCACCCTCA	GCATGA		886

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 898 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (C) INDIVIDUAL ISOLATE: Lelystad
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGGAGGCC TAGACGATTT TTGCAACGAT CCTATCGCCG CACAAAAGCT CGTGCTAGCC 60

TTTAGCATCA	CATACACACC	TATAATGATA	TACGCCCTTA	AGGTGTCACG	CGGCCGACTC	120
CTGGGGCTGT	TGCACATCCT	AATATTTCTG	AACTGTTCCT	TTACATTCGG	ATACATGACA	180
TATGTGCATT	TTCAATCCAC	CAACCGTGTC	GCACTTACCC	TGGGGGCTGT	TGTCGCCCTT	240
CTGTGGGGTG	TTTACAGCTT	CACAGAGTCA	TGGAAGTTTA	TCACTTCCAG	ATGCAGATTG	300
TGTTGCCTTG	GCCGGCGATA	CATTCTGGCC	CCTGCCCATC	ACGTAGAAAG	TGCTGCAGGT	360
CTCCATTCAA	TCTCAGCGTC	TGGTAACCGA	GCATACGCTG	TGAGAAAGCC	CGGACTAACA	420
TCAGTGAACG	GCACTCTAGT	ACCAGGACTT	CGGAGCCTCG	TGCTGGGCGG	CAAACGAGCT	480
GTTAAACGAG	GAGTGGTTAA	CCTCGTCAAG	TATGGCCGGT	AAAAACCAGA	GCCAGAAGAA	540
AAAGAAAAGT	ACAGCTCCGA	TGGGGAATGG	CCAGCCAGTC	AATCAACTGT	GCCAGTTGCT	600
GGGTGCAATG	ATAAAGTCCC	AGCGCCAGCA	ACCTAGGGGA	GGACAGGCCA	AAAAGAAAAA	660
GCCTGAGAAG	CCACATTTTC	CCCTGGCTGC	TGAAGATGAC	ATCCGGCACC	ACCTCACCCA	720
GACTGAACGC	TCCCTCTGCT	TGCAATCGAT	CCAGACGGCT	TTCAATCAAG	GCGCAGGAAC	780
TGCGTCGCTT	TCATCCAGCG	GGAAGGTCAG	TTTTCAGGTT	GAGTTTATGC	TGCCGGTTGC	840
TCATACAGTG	CGCCTGATTC	GCGTGACTTC	TACATCCGCC	AGTCAGGGTG	CAAGTTAA	898

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-1894
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG Met 1	GTA	TCG Ser	TCC Ser	TTA Leu 5	. Asp	GAC Asp	TTC Phe	TGC Cys	CAT His	Asp	AGT Sei	ACG Thi	GCT c Ala	CCA Pro	Gln	48
AAG Lys	GTG Val	CTT Leu	TTG Leu 20	Ala	TTT Phe	TCT Ser	ATT	ACC Thr 25	· Tyr	ACG Thr	CCA Pro	GTG Val	ATG L Met 30	Ile	TAT Tyr	96
GCC Ala	CTA Leu	AAG Lys 35	GTG Val	AGT Ser	CGC Arg	GGC Gly	CGA Arg 40	Leu	CTA Leu	GGG Gly	CTT Leu	CTG Leu 45		CTT Leu	TTG Leu	144
ATC Ile	TTC Phe 50	CTG Leu	AAT Asn	TGT Cys	GCT Ala	TTC Phe 55	ACC Thr	TTC Phe	GGG Gly	TAC Tyr	ATG Met 60	Thr	TTC Phe	GTG Val	CAC His	192
TTT Phe 65	CAG Gln	AGT Ser	ACA Thr	AAT Asn	AAG Lys 70	GTC Val	GCG Ala	CTC Leu	ACT Thr	ATG Met 75	Gly	GCA Ala	GTA Val	GTT Val	GCA Ala 80	240
CTC Leu	CTT Leu	TGG Trp	GGG Gly	GTG Val 85	TAC Tyr	TCA Ser	GCC Ala	ATA Ile	GAA Glu 90	ACC Thr	TGG Trp	AAA Lys	TTC Phe	ATC Ile 95	Thr	288
TCC Ser	AGA Arg	TGC Cys	CGT Arg 100	TTG Leu	TGC Cys	TTG Leu	CTA Leu	GGC Gly 105	CGC Arg	AAG Lys	TAC Tyr	ATT Ile	CTG Leu 110	GCC Ala	CCT Pro	336
GCC Ala	CAC His	CAC His 115	GTT Val	GAA Glu	AGT Ser	GCC Ala	GCA Ala 120	GGC Gly	TTT Phe	CAT His	CCG Pro	ATT Ile 125		GCA Ala	AAT Asn	384
GAT Asp	AAC Asn 130	CAC His	GCA Ala	TTT Phe	GTC Val	GTC Val 135	CGG Arg	CGT Arg	CCC Pro	GGC Gly	TCC Ser 140	ACT Thr	ACG Thr	GTC Val	AAC Asn	432
GGC Gly 145	ACA Thr	TTG Leu	GTG Val	CCC Pro	GGG Gly 150	TTG Leu	AAA Lys	AGC Ser	CTC Leu	GTG Val 155	TTG Leu	GGT Gly	GGC Gly	AGA Arg	AAA Lys 160	480
GCT Ala	GTT Val	AAA Lys	CAG Gln	GGA Gly 165	GTG Val	GTA Val	AAC Asn	CTT Leu	GTC Val 170	AAA Lys	TAT Tyr	GCC Ala	AAA Lys			522
TAA			,													525

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln
1 10 15

Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr 20 25 30

Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu 35 40 45

Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His 50 55 60

Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala 65 70 75 80

Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr 85 90 95

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro 100 105 110

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn 115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn 130 135 140

Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys 145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys 165 170

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear

(ii) MOLECULE	TYPE:	cDNA
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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATG Met 1	GGG Gly	TCG Ser	TCC Ser	TTA Leu 5	GAT Asp	GAC Asp	TTC Phe	TGT Cys	CAT His 10	Asp	AGC Ser	ACG Thr	GCT Ala	CCA Pro 15	Gln	48
AAG Lys	GTG Val	CTT Leu	TTG Leu 20	GCG Ala	TTT Phe	TCT Ser	ATT Ile	ACC Thr 25	TAC Tyr	ACG Thr	CCA Pro	GTG Val	ATG Met 30	Ile	TAT Tyr	96
GCC Ala	CTG Leu	AAG Lys 35	GTG Val	AGT Ser	CGC Arg	GGC Gly	CGA Arg 40	CTG Leu	CTA Leu	GGG Gly	CTT Leu	CTG Leu 45	His	CTT Leu	TTG Leu	144
ATC Ile	TTC Phe 50	CTG Leu	AAT Asn	TGT Cys	GCT Ala	TTC Phe 55	ACC Thr	TTC Phe	GGG Gly	TAC Tyr	ATG Met 60	Thr	TTC Phe	GTG Val	CAC His	192
TTT Phe 65	CAG Gln	AGT Ser	ACA Thr	AAT Asn	AAG Lys 70	GTC Val	GCA Ala	CTC Leu	ACT Thr	ATG Met 75	GGA Gly	GCA Ala	GTA Val	GTT Val	GCA Ala 80	240
						TCA Ser									Thr	288
						TTG Leu								Ala	CCT Pro	336
						GCC Ala							Ala		AAT Asn	384
GAT Asp	AAC Asn 130	CAC His	GCA Ala	TTT Phe	GTC Val	GTT Val 135	CGG Arg	CGT Arg	CCC Pro	GGC Gly	TCC Ser 140	Thr	ACG Thr	GTC Val	AAC Asn	432

Gly 145	Thr	Leu	Val	Pro	Gly 150	Leu	Lys	Ser	Leu	Val 155	Leu	Gly	Gly	Arg	Lys 160
GCT Ala	GTT Val	AAA Lys	CAG Gln	GGA Gly 165	GTG Val	GTA Val	AAC Asn	CTT Leu	GTC Val 170	AAA Lys	TAT Tyr	GCC Ala	AAA Lys		
TAA															
(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:4!	5:				**			
		(i) :		LEI TYI	NGTH PE: 8	: 174 amino	ERIST 4 am: o ac: linea	ino a id		5		-			
	. (:	ii) 1	MOLE	CULE	TYPI	E: p	rote	in							
	(2	xi) s	SEQUI	ENCE	DES	CRIP:	rion	: SE(Q ID	NO:	45:				
Met 1	Gly	Ser	Ser	Leu 5	Asp.	Asp	Phe	Cys	His 10	Asp	Ser	Thr	Ala	Pro 15	Gln
Lys	Val	Leu	Leu 20	Ala	Phe	Ser	Ile	Thr 25	Tyr	Thr	Pro	Val	Met 30	Ile	Tyr
Ala	Leu	Lys 35	Val	Ser	Arg	Gly	Arg 40	Leu	Leu	Gly	Leu	Leu 45	His	Leu	Leu
Ile	Phe 50	Leu	Asn	Cys	Ala	Phe 55	Thr	Phe	Gly	Tyr	Met 60	Thr	Phe	Val	His
Phe 65	Gln	Ser	Thr	Asn	Lys 70	Val	Ala	Leu	Thr	Met 75	Gly	Ala	Val	Val	Ala 80
Leu	Leu	Trp	Gly	Val 85	Tyr	Ser	Ala	Ile	Glu 90	Thr	Trp	Lys	Phe	Ile 95	Thr
Ser	Arg	Cys	Arg 100	Leu	Cys	Leu	Leu	Gly 105	Arg	Lys	Tyr	Ile	Leu 110	Ala	Pro
Ala	His	His 115	Val	Glu	Ser	Ala	Ala 120	Gly	Phe	His	Pro	Ile 125	Ala	Ala	Asn
Asp	Asn 130	His	Ala	Phe	Val	Val 135	Arg	Arg	Pro	Gly	Ser 140	Thr	Thr	Val	Asn
Gly 145	Thr	Leu	Val	Pro	Gly 150	Leu	Lys	Ser	Leu	Val 155	Leu	Gly	Gly	Arg	Lys 160

Ala	Val	Lys	Gln	Gly	Val	Val	Asn	Leu	Val	Lys	Tyr	Ala	Lys
				165					170		_		-

(2) INFORMATION FOR SEQ ID NO:	46	NO:	·ID	SEQ	FOR	INFORMATION	(2)	(
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-79
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATG Met 1	GGG Gly	TCG Ser	TCC Ser	TTA Leu 5	GAT Asp	GAC Asp	TTC Phe	TGT Cys	TAT Tyr 10	GAT Asp	AGT Ser	ACG Thr	GCT Ala	CCA Pro 15	CAA Gln	48
AAG Lys	GTG Val	CTT Leu	TTG Leu 20	GCA Ala	TTT Phe	TCT Ser	ATT Ile	ACC Thr 25	TAC Tyr	ACG Thr	CCA Pro	GTA Val	ATG Met 30	ATA Ile	TAT Tyr	96
GCC Ala	CTA Leu	AAG Lys 35	GTG Val	AGT Ser	CGC Arg	GGC Gly	CGA Arg 40	CTG Leu	CTA Leu	GGG Gly	CTT Leu	CTG Leu 45	CAC His	CTT Leu	TTG Leu	144
ATT Ile	TTC Phe 50	CTG Leu	AAC Asn	TGT Cys	GCT Ala	TTC Phe 55	ACC Thr	TTC Phe	GGG Gly	TAC Tyr	ATG Met 60	ACA Thr	TTC Phe	ATG Met	CAC His	192
TTT Phe 65	CAG Gln	AGT Ser	ACA Thr	AAT Asn	AAG Lys 70	GTC Val	GCG Ala	CTC Leu	ACT Thr	ATG Met 75	GGA Gly	GCA Ala	GTA Val	GTT Val	GCA Ala 80	240
CTC Leu	CTT Leu	TGG Trp	GGG Gly	GTG Val 85	TAC Tyr	TCA Ser	GCC Ala	ATA Ile	GAA Glu 90	ACC Thr	TGG Trp	AAA Lys	TTC . Phe	ATC . Ile 95	ACC Thr	. 288

Ser	AGA Arg	TGC Cys	CGT Arg 100	TTG Leu	TGC Cys	TTG Leu	CTA Leu	GGC Gly 105	CGC Arg	AAG Lys	TAC Tyr	ATT Ile	CTG Leu 110	GCC Ala	CCT Pro
GCC Ala	CAC His	CAC His 115	GTT Val	GAA Glu	AGT Ser	GCC Ala	GCA Ala 120	GGC Gly	TTT Phe	CAT His	CCG Pro	ATT Ile 125	GCG Ala	GCA Ala	AAT Asn
GAT Asp	AAC Asn 130	CAC His	GCA Ala	TTT Phe	GTC Val	GTC Val 135	CGG Arg	CGT Arg	CCC Pro	GGC Gly	TCC Ser 140	ACT Thr	ACG Thr	GTC Val	AAC Asn
GGC Gly 145	ACA Thr	TTG Leu	GTG Val	CCC Pro	GGG Gly 150	TTG Leu	AAA Lys	AGC Ser	CTC Leu	GTG Val 155	TTG Leu	GGT Gly	GGC Gly	AGA Arg	AAA Lys 160
GCT Ala	GTT Val	AAA Lys	CAG Gln	GGA Gly 165	GTG Val	GTA Val	AAC Asn	CTT Leu	GTC Val 170	AAA Lys	TAT Tyr	GCC Ala	AAA Lys		
TAA															,
(2)	INFO	ORMAT	rion	FOR	SEQ	ID 1	NO : 4 T	7:							
		(i) S	SEQUE	ENCE	CHAI	RACTI	ERIST	rics	•						
				LEI TYI TOI		amino	ami	ino a id		3					
	i)	Li) N	(B)	TYI	PE: a	amino 3Y:]	ami aci linea	ino a id ar		5		, .		,	
		·	(B) (D)	TYI TOI CULE	PE: 6 POLOC TYPE	amino EY:]	ami o aci linea	ino a id ar in	acid		17:	, ,			
Met 1	()	ci) S	(B) (D) MOLEC	TYI TOI CULE	PE: a POLOC TYPE DESC	amino Ey:] E: p:	ami o aci linea cotei	ino a id ar in : SE(acids	NO : 4		Thr	Ala	Pro 15	Gln
1	() Gly	ci) S Ser Leu	(B) (D) MOLEC	TYPE TOPE TOPE TOPE TOPE TOPE TOPE TOPE TO	PE: 6 POLOC TYPE DESC Asp	amind GY:] E: pr CRIP? Asp	and action action action action action actions.	ino a id ar in : SE(Q ID Tyr 10	NO:4	Ser			15	
Lys	() Gly Val	ci) S Ser Leu	(B) (D) (OLEC SEQUE Ser Leu 20	TYI TOI CULE ENCE Leu 5	PE: 6 POLOG TYPE DESG Asp Phe	amind GY:] E: pr CRIPT Asp Ser	1 amic acidinea linea cotei TION: Phe	ino aid ar in SEQ Cys	Q ID Tyr 10	NO:4	Ser Pro	Val	Met 30	15 Ile	
Lys Ala	() Gly Val Leu	Ser Leu Lys 35	(B) (D) (OLEC SEQUE Ser Leu 20	TYPE TOPE CULE ENCE Leu 5 Ala	PE: a POLOG TYPE DESG Asp Phe	amind GY:] E: pr CRIPT Asp Ser	1 amic acidines Cotei FION: Phe Ile Arg 40	ino a id ar in SEC Cys Thr 25	Q ID Tyr 10 Tyr	NO:4 Asp Thr	Ser Pro Leu	Val Leu 45	Met 30 His	15 Ile Leu	Tyr Leu
Lys Ala Ile	Gly Val Leu Phe 50	Ser Leu Lys 35 Leu	(B) (D) (OLEC SEQUE Ser Leu 20 Val	TYI TOI CULE ENCE Leu 5 Ala Ser Cys	PE: a POLOC TYPE DESC Asp Phe Arg	Amino GY:] E: pr CRIPT Asp Ser Gly Phe 55	1 amic acidines Lines FION: Phe Ile Arg 40 Thr	ino aid ar in Cys Thr 25 Leu Phe	Tyr 10 Tyr Leu Gly	NO:4 Asp Thr Gly	Ser Pro Leu Met 60	Val Leu 45 Thr	Met 30 His	15 Ile Leu Met	Tyr Leu His

Ser	Arg	Cys	Arg 100	Leu	Cys	Leu	Leu	Gly 105	Arg	Lys	Tyr	Ile	Leu 110	Ala	Pro		
Ala	His	His 115	Val	Glu	Ser	Ala	Ala 120	Gly	Phe	His	Pro	Ile 125	Ala	Ala	Asn		
Asp	Asn 130	His	Ala	Phe	Val	Val 135	Arg	Arg	Pro	Gly	Ser 140	Thr	Thr	Val	Asn	·	
Gly 145	Thr	Leu	Val	Pro	Gly 150	Leu	Lys	Ser	Leu	Val 155	Leu	Gly	Gly	Arg	Lys 160		
Ala	Val	Lys	Gln	Gly 165	Val	Val	Asn	Leu	Val 170	Lys	Tyr	Ala	Lys	,			
(2)	INFO	DRMAT	CION	FOR	SEQ	ID N	10:48	3:									•
	(i)	(E	A) LE 3) TY C) ST	ENGTI PE : RANI	I: 52 nuc] EDNI	CTERI 25 ba leic ESS: line	se p acid unkr	oairs l	3							•	
	(ii)	MOI	ECUI	Æ TY	PE:	cDNA			,								
	(vi)	(E	A) OR B) SI	GANI vir RAIN	SM: Tus J: Ic	porc							pira	itory	sync	lrome	è
	(ix)		AN (A	ME/K		CDS 15	22							. •	·		
	(xi)	SEQ	UENC	E DE	SCRI	PTIC	N: S	EQ I	D NC	:48:							
ATG Met 1	GGG Gly	TCG Ser	TCC Ser	TTA Leu 5	GAT Asp	GAC ' Asp	TTC T	IGC (Cys	CAT (His 10	ASP	AGC <i>I</i> Ser	ACG (Thr	CT (Ala	CA C Pro 15	AA Gln	•	48
AAG Lys	GTG Val	CTT . Leu	TTG Leu 20	GCG Ala	TTC Phe	TCT : Ser	ATT I	ACC Thr 25	FAC <i>I</i> Tyr	ACG (Thr	CCA (Pro	TG <i>F</i> Val	ATG A Met 30	TA T	'AT Tyr		96
GCC Ala	CTA Leu	AAA Lys 35	GTA . Val	AGT Ser	CGC Arg	GGC (Gly	CGA (Arg 40	CTG (Leu	CTA (Leu	GG (CTT (Leu	TG C Leu 45	AC C	TT T Leu	TG Leu		144

										CAC His	192
							Gly	GCA Ala		GCA Ala 80	240
								AAA Lys		ACC Thr	 288
								ATT Ile		CCT Pro	336
								ATA Ile 125		AAT Asn	384
	•									AAC Asn	432
							Leu	GGT Gly		AAA Lys 160	480
						Lys		GCC Ala			522
TAA		- '						٠			525

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln
1 5 10 15

Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr 20 25 30

Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu 35 40 45

Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His 50 55 60

Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala 65 70 75 80

Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr 85 90 95

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro 100 105 110

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn 115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn 130 135 140

Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys 145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
165 170

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATG Met 1	GTA	TCG Ser	TCC Ser	CTA Leu 5	GAC Asp	GAC Asp	TTT Phe	TGC Cys	AAT Asr	ı Asp	AGC Sei	ACG Th:	GCT r Ala	CCA a Pro 1!	CAA o Gln 5	48
AAG Lys	GTG Val	CTT Leu	TTG Leu 20	Ата	TTT Phe	TCT Ser	ATT Ile	ACC Thr 25	. Tyr	ACG Thr	CCG Pro	GTG Val	ATG L Met	: Il ϵ	TAT Tyr	96
GCT Ala	CTA Leu	AAG Lys 35	GTA Val	AGT Ser	CGC Arg	GGC Gly	CGA Arg 40	Leu	CTA Leu	GGG Gly	CTT Leu	CTG Let 45	ı His	CTT Let	TTG 1 Leu	144
ATT Ile	TTT Phe 50	CTG Leu	AAT Asn	TGT Cys	GCT Ala	TTT Phe 55	ACT Thr	TTC Phe	GGG Gly	TAC Tyr	ATG Met	Thr	TTC Phe	GTG Val	CAC His	192
TTT Phe 65	GAG Glu	AGC Ser	ACA Thr	AAT Asn	AGG Arg 70	GTC Val	GCG Ala	CTC Leu	ACT Thr	ATG Met 75	Gly	GCA Ala	GTA Val	GTC Val	GCA Ala 80	240
CTT Leu	CTC Leu	TGG Trp	GGG Gly	GTG Val 85	TAC Tyr	TCA Ser	GCC Ala	ATA Ile	GAA Glu 90	ACC Thr	TGG Trp	AAA Lys	TTC Phe	ATC Ile	Thr	288
TCC Ser	AGA Arg	TGC Cys	CGT Arg 100	TTG Leu	TGC Cys	TTG Leu	CTA Leu	GGC Gly 105	CGC Arg	AAG Lys	TAC Tyr	ATT Ile	CTG Leu 110	Ala	CCT Pro	336
GCC Ala	CAC His	CAC His 115	GTT Val	GAG Glu	AGT Ser	GCC Ala	GCA Ala 120	GGC Gly	TTT Phe	CAT His	CCG Pro	ATT Ile 125	Ala	GCA Ala	AAT Asn	384
GAT Asp	AAC Asn 130	CAC His	GCA Ala	TTT Phe	GTC Val	GTC Val 135	CGG Arg	CGT Arg	CCC Pro	GGC Gly	TCC Ser 140	ACT Thr	ACG Thr	GTT Val	AAC Asn	432
GGC Gly 145	ACA Thr	TTG Leu	GTG Val	CCC Pro	GGG Gly 150	TTG . Leu	AGA Arg	AGC Ser	CTC Leu	GTG Val 155	TTG Leu	GGT Gly	GGC Gly	AAA Lys	AAA Lys 160	480
GCT Ala	GTT Val	AAG Lys	CAG Gln	GGA Gly 165	GTG Val	GTA . Val	AAC Asn	CTT Leu	GTT Val 170	AAA Lys	TAT Tyr	GCC Ala	AAA Lys			522
TAA																525

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
- Met Gly Ser Ser Leu Asp Asp Phe Cys Asn Asp Ser Thr Ala Pro Gln
 1 5 10 15
- Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr 20 25 30
- Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu 35 40 45
- Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His 50 60
- Phe Glu Ser Thr Asn Arg Val Ala Leu Thr Met Gly Ala Val Val Ala 65 70 75 80
- Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr 85 90 95
- Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro 100 105 110
- Ala His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn 115 120 125
- Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn 130 135 140
- Gly Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Lys 145 150 155 160
- Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
 165 170
- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-1894

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATG Met 1	CCA Pro	AAT Asn	AAC Asn	AAC Asn 5	GGC Gly	AAG Lys	CAG Gln	CAG Gln	AAG Lys 10	AGA Arg	AAG Lys	AAG Lys	GGG Gly	GAT Asp 15	GGC Gly	48
CAG Gln	CCA Pro	GTC Val	AAT Asn 20	CAG Gln	CTG Leu	TGC Cys	CAG Gln	ATG Met 25	CTG Leu	GGT Gly	AAG Lys	ATC Ile	ATC Ile 30	Ala	CAG Gln	96
CAA Gln	AAC Asn	CAG Gln 35	TCC Ser	AGA Arg	GGC Gly	AAG Lys	GGA Gly 40	CCG Pro	GGA Gly	AAG Lys	AAA Lys	AAC Asn 45	AAG Lys	AAG Lys	AAA Lys	· 144
AAC Asn	CCG Pro 50	GAG Glu	AAG Lys	CCC Pro	CAT His	TTT Phe 55	CCT Pro	CTA Leu	GCG Ala	ACT Thr	GAA Glu 60	GAT Asp	GAT Asp	GTC Val	AGA Arg	192
CAT His 65	CAC His	TTC Phe	ACC Thr	CCT Pro	AGT Ser 70	GAG Glu	CGG Arg	CAA Gln	TTG Leu	TGT Cys 75	CTG Leu	TCG Ser	TCA Ser	ATC Ile	CAG Gln 80	240
ACC Thr	GCC Ala	TTT Phe	AAT Asn	CAA Gln 85	GGC Gly	GCT Ala	GGG Gly	ACT Thr	TGC Cys 90	ACC Thr	CTG Leu	TCA Ser	GAT Asp	TCA Ser 95	GGG Gly	288
AGG Arg	ATA Ile	AGT Ser	TAC Tyr 100	ACT Thr	GTG Val	GAG Glu	TTT Phe	AGT Ser 105	TTG Leu	CCA Pro	ACG Thr	CAT His	CAT His 110	ACT (GTG Val	336
CGC Arg	TTG Leu	ATC Ile 115	CGC Arg	GTC Val	ACA Thr	GCA Ala	TCA Ser 120	CCC Pro	TCA Ser	GCA Ala	TGA	,				372

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Pro Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly
1 5 10 15

Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln 20 25 30

Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys 35 40 45

Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg 50 55 60

His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln 65 70 75 80

Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly
85 90 95

Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val

Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala 115 120

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

1	'ix'	FEATURE
١		LUAIURE

(A) NAME/KEY: CDS

(B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATG Met 1	CCA Pro	AAT Asn	AAC Asn	AAC Asn 5	GGT Gly	AAG Lys	CAG Gln	CAG Gln	AAG Lys 10	Arg	AAG Lys	AAG Lys	GGG Gly	GAT Asp 15	GGC Gly	48
CAG Gln	CCA Pro	GTC Val	AAT Asn 20	CAG Gln	CTG Leu	TGC Cys	CAG Gln	ATG Met 25	CTG Leu	GGC Gly	AAG Lys	ATC Ile	ATC Ile 30	GCT Ala	CAG Gln	96
CAA Gln	AAT Asn	CAG Gln 35	TCC Ser	AGA Arg	GGC Gly	AAG Lys	GGA Gly 40	CCG Pro	GGA Gly	AAG Lys	AAA Lys	AAT Asn 45	AAG . Lys	AAG 1 Lys	AAA Lys	144
AAC Asn	CCG Pro 50	GAG Glu	AAG Lys	CCC Pro	CAT His	TTT Phe 55	CCT Pro	CTA Leu	GCG Ala	ACT Thr	GAA Glu 60	GAT Asp	GAT Asp	GTC A	AGA Arg	192
CAT His 65	CAC His	TTT Phe	ACC Thr	CCT Pro	AGT Ser 70	GAG Glu	CGG Arg	CAA Gln	TTG Leu	TGT Cys 75	CTG Leu	TCG Ser	TCA Z Ser	ATC (Ile	CAG Gln 80	240
ACC Thr	GCC Ala	TTT Phe	AAT Asn	CAA Gln 85	GGC Gly	GCT Ala	GGG Gly	ACT Thr	TGC Cys 90	ACC Thr	CTG Leu	TCA Ser	GAT ' Asp	FCA (Ser 95	GG Gly	288
AGG Arg	ATA Ile	AGT Ser	TAC Tyr 100	ACT Thr	GTG Val	GAG Glu	TTT Phe	AGT Ser 105	TTG Leu	CCT Pro	ACG Thr	CAT His	CAT A His 110	ACT (TG Val	336
CGC Arg	CTG Leu	ATC Ile 115	CGC Arg	GTC Val	ACA Thr	GCA Ala	TCA Ser 120	CCC Pro	TCA Ser	GCA Ala	TGA				-	372

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Pro Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly
1 5 10 15

Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln 20 25 30

Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys 35 40 45

Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg 50 55 60

His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln 65 70 75 80

Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly 85 90 95

Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val 100 105 110

Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala 115 120

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-79
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

48	AAG GGG GAT GGC s Lys Gly Asp Gly 15	A AAG cg Lys	AG AG Lys A: 10	CAG Gln	CAG Gln	AAG Lys	GGC Gly	AAC Asn 5	AAC Asn	AAT Asn	CCA Pro	ATG Met 1
96	ATC ATC GCC CAG s Ile Ile Ala Gln 30	T AAG Ly Lys	TG GG Leu Gl	ATG Met 25	CAG Gln	TGC Cys	CTG Leu	CAG Gln	AAT Asn 20	GTC Val	CCA Pro	CAG Gln
144	AAT AAG AAG AAA s Asn Lys Lys Lys 45	G AAA ⁄s Lys	GA AA Gly Ly	CCG Pro	GGA Gly 40	AAG Lys	GGC Gly	AGA Arg	TCT Ser	CAG Gln 35	AAC Asn	CAA Gln
. 192	GAT GAT GTC AGA 1 Asp Asp Val Arg)	T GAA nr Glu 60	CG AC Ala Ti	CTA Leu	CCT Pro	TTT Phe 55	CAT His	CCC Pro	AAG Lys	GAG Glu	CCG Pro 50	AAC Asn
240	TCG TCA ATC CAA 1 Ser Ser Ile Gln 80	r CTG 's Leu '5	Leu Cy	CAA Gln	CGG Arg	GAG Glu	AGT Ser 70	CCT Pro	ACC Thr	TTT Phe	CAC His	CAT His 65
288	TCA GAT TCA GGG 1 Ser Asp Ser Gly 95	C CTG ir Leu	GC AC Cys Th 90	ACT Thr	GGG Gly	GCT Ala	GGC Gly	CAA Gln 85	AAT Asn	TTT Phe	GCC Ala	ACT Thr
336	CAT CAT ACT GTG His His Thr Val	F ACG o Thr	TG CC Leu Pr	AGT Ser 105	TTT Phe	GAG Glu	GTG Val	ACT Thr	TAC Tyr 100	AGT Ser	ATA Ile	AGG Arg
372		A TGA a	CA GC Ser Al	CCC Pro	TCA Ser 120	GCA Ala	ACA Thr	GTC Val	CGC Arg	ATC Ile 115	TTG Leu	CGC Arg

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids

 - (B) TYPE: amino acid (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Pro Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly

Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln 20 25 .

Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys
35 40 45

Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg 50 55 60

His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln 65 70 75 80

Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly 85 90 95

Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val

Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala 115 120

- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus

- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..369
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
- CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAG

 Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln

 20

 25

 30

CAA Gln	AAC Asn	CAG Gln 35	TCC Ser	AGA Arg	GGC Gly	AAG Lys	GGA Gly 40	Pro	GGA Gly	AAG Lys	AAA Lys	AAC Asr 45	Lys	AAG Lys	AAA Lys	3	144
AAC Asn	CCG Pro 50	GAG Glu	AAG Lys	CCC Pro	CAT His	TTT Phe 55	CCT Pro	CTA Leu	GCG Ala	ACT Thr	GAA Glu 60	Asp	GAT Asp	GTC Val	AGA Arg	ſ	192
CAT His 65	CAC His	TTC	ACC Thr	TCT Ser	GGT Gly 70	GAG Glu	CGG Arg	CAA Gln	TTG Leu	TGT Cys 75	CTG Leu	TCG Ser	TCA Ser	ATC Ile	CAG Gln 80		240
ACA Thr	GCC Ala	TTT Phe	AAT Asn	CAA Gln 85	GGC Gly	GCT Ala	GGA Gly	ACT Thr	TGT Cys 90	Thr	CTG Leu	TCA Ser	GAT Asp	TCA Ser 95	Gly		288
AGG Arg	ATA Ile	AGT Ser	TAC Tyr 100	ACT Thr	GTG Val	GAG Glu	TTT Phe	AGT Ser 105	TTG Leu	CCG Pro	ACG Thr	CAT His	CAT His 110	Thr	GTG Val		336
CGC Arg	TTG Leu	ATC Ile 115	CGC Arg	GTC Val	ACA Thr	GCG Ala	TCA Ser 120	CCC Pro	TCA Ser	GCA Ala	TGA						372
(2)	INFO	ORMAT	CION	FOR	SEQ	ID N	10:59	€:									
	. ((i) S	(A) (B)	LEN TYF	IGTH: PE: a	RACTE : 123 amino SY: 1	ami aci	ino a id	: acids	5							
	(i	.i) M	OLEC	ULE	TYPE	: pr	otei	.n									
	(x	i) S	EQUE	NCE	DESC	RIPT	'ION :	SEÇ) ID	NO:5	59:		-				
Met 1	Pro	Asn	Asn .	Asn 5	Gly	Lys	Gln	Gln	Lys 10	Lys	Lys	Lys	Gly	Asp 15	Gly		,
Gln	Pro	Val	Asn 20	Gln	Leu	Cys	Gln	Met 25	Leu	Gly	Lys	Ile	Ile 30	Ala	Gln		
Gl'n	Asn	Gln 35	Ser .	Arg	Gly	Lys	Gly 40	Pro	Gly	Lys	Lys	Asn	Lys	Lys	Lys		

Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg

His His Phe Thr Ser Gly Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln 65 70 75 80

Thr	Ala	Phe	Asn	. Gln 85	Gly	Ala	Gly	Thr	Cys 90	Thr	Leu	Ser	Asp	Ser 95	Gly	
Arg	Ile	Ser	Tyr 100	Thr	Val	Glu	Phe	Ser 105	Leu	Pro	Thr	His	His 110	Thr	Val	
Arg	Leu	Ile 115	Arg	Val	Thr	Ala	Ser 120	Pro	Ser	Ala						
(2)	INF	ORMA'	TION	FOR	SEQ	ID	NO:60	O: .								
	(i)	() () ()	A) L B) T C) S	ENGTI YPE : TRANI	H: 3 nuc DEDN	CTER 72 ba leic ESS: line	ase p acio unkr	pairs 1	5			••				
•	(ii)	MO1	LECU:	LE T	YPE:	CDNA	Ž ·					•				
									•							
·		(I (C FE <i>I</i>	A) O1 B) S' C) II ATURI	VII TRAIN NDIVI	(SM: cus V: IOUA	pord owa L ISC								tory	sync	lrome
				AME/K DCATI		CDS 13	69									
	(xi)	SEC	UENC	CE DE	SCR	IPTIC	N: S	EQ I	D NO	:60:						
ATG Met 1	CCA Pro	AAT Asn	AAC Asn	AAC Asn 5	GGC Gly	AAG Lys	CAG (Gln	CAG /	AAG <i>I</i> Lys 10	AAA <i>I</i> Lys	AAG A Lys	AG C Lys	GG G	AT G Asp 15	GC Gly	48
CAG Gln	CCA Pro	GTC Val	AAT Asn 20	CAG Gln	CTC Leu	TGC (Cys	CAA <i>l</i> Gln	ATG (Met 25	CTG C Leu	GT A	AAG A Lys	TC A Ile	TC G Ile 1 30	CC C Ala	AG Gln	96
CAA Gln	AAC Asn	CAG Gln 35	TCC Ser	AGA (Arg	GGT Gly	AAG (Lys	GGA (Gly 40	CCG G Pro	GA A	AG A Lys	AA A Lys .	AT A Asn : 45	AG A Lys :	AG A Lys	AA Lys	144
AAC Asn	CCG Pro 50	GAG : Glu	AAG Lys	CCC (Pro	CAT His	TTT (Phe 55	CCT (Pro	CTA C Leu .	CG A Ala '	CT G	AA G Glu 60	AT G Asp	AT G' Asp '	TC A	GA Arg	192

His 65	2 IITS	Phe	F Thr	Pro	Ser 70	GIU	CGG Arg	CAA Glr	TTG Leu	TGT Cys 75	Leu	TCG Sei	TCA Sei	ATC : Ile	CAG e Gln 80
ACT Thi	GCC Ala	TTT Phe	AAT Asn	CAG Gln 85	гету	GCT Ala	GGG Gly	ACC Thr	TGT Cys 90	Ile	CTA Leu	TCA Ser	GAT Asp	TCA Ser	GGG Gly
AGC Arg	ATA	AGT Ser	TAC Tyr 100	TIII	GTG Val	GAG Glu	TTT Phe	AGT Ser 105	Leu	CCG Pro	ACG Thr	CAT His	CAT His	Thr	GTG Val
CGC Arg	CTG Leu	ATT Ile	' CGC Arg	GTC Val	ACG Thr	GCA Ala	CCA Pro 120	Pro	TCA Ser	GCA Ala	TGA				
(2)	INF	ORMA	TION	FOR	SEQ	ID :	NO:6	1:							
		(i)	(B) LE:) TY:	CHA NGTH PE: POLO	: 12	3 am.	ino . id	: acid	S					
	(ii)	MOLE	CULE	TYP	E: p:	rote	in							•
	(:	xi)	SEQU		DES		PION	: SE	QID	NO : 6	51:				
Met 1			SEQUI	ENCE		CRIP						Lys	Gly	Asp 15	Gly
-	Pro	Asn	SEQUI Asn	ENCE Asn 5	Gly	CRIP'	Gln	Gln	Lys 10	Lys	Lys			15	Gly
Gln	Pro	Asn Val	SEQUI Asn Asn	ENCE Asn 5 Gln	Gly Leu	CRIP Lys Cys	Gln Gln	Gln Met 25	Lys 10 Leu	Lys Gly	Lys	Ile	Ile 30	15 Ala	Gln
Gln	Pro Pro Asn	Asn Val Gln 35	Asn Asn 20	Asn 5 Gln Arg	Gly Leu Gly	CRIP: Lys Cys Lys	Gln Gln Gly 40	Gln Met 25 Pro	Lys 10 Leu Gly	Lys Gly Lys	Lys Lys Lys	Ile Asn 45 Asp	Ile 30 Lys	15 Ala Lys	Gln Lys
Gln Gln Asn	Pro Pro Asn Pro 50	Asn Val Gln 35 Glu	Asn Asn 20 Ser	Asn 5 Gln Arg Pro	Gly Leu Gly His	Lys Cys Lys Phe	Gln Gly 40 Pro	Gln Met 25 Pro	Lys 10 Leu Gly	Lys Gly Lys Thr	Lys Lys Lys Glu 60	Ile Asn 45 Asp	Ile 30 Lys Asp	15 Ala Lys Val	Gln Lys Arg
Gln Gln Asn His	Pro Pro Asn Pro 50 His	Asn Val Gln 35 Glu Phe	Asn Asn 20 Ser	Asn 5 Gln Arg Pro	Gly Leu Gly His Ser 70	Lys Cys Lys Phe 55	Gln Gly 40 Pro	Gln Met 25 Pro Leu Gln	Lys 10 Leu Gly Ala Leu	Lys Gly Lys Thr Cys 75	Lys Lys Lys Glu 60 Leu	Ile Asn 45 Asp Ser	Ile 30 Lys Asp	15 Ala Lys Val	Gln Lys Arg
Gln Gln Asn His 65	Pro Pro Asn Pro 50 His	Asn Val Gln 35 Glu Phe	Asn Asn 20 Ser Lys	Asn 5 Gln Arg Pro Pro Gln 85	Gly Leu Gly His Ser 70 Gly	Lys Cys Lys Phe 55 Glu Ala	Gln Gly 40 Pro Arg Gly	Gln Met 25 Pro Leu Gln Thr	Lys 10 Leu Gly Ala Leu Cys 90	Lys Gly Lys Thr Cys 75	Lys Lys Glu 60 Leu Leu	Ile Asn 45 Asp Ser	Ile 30 Lys Asp Ser	15 Ala Lys Val Ile Ser 95	Gln Lys Arg Gln 80 Gly

- (2) INFORMATION FOR SEQ ID NO:62:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Lys Lys Ser Thr Ala Pro Met 1 5

- (2) INFORMATION FOR SEQ ID NO:63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Ser Gln Gly

- (2) INFORMATION FOR SEQ ID NO:64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: DNA (synthetic)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
TCTTCTTGCC TTTTCTATGC TTCTGAGATG AGTGAAAAGG GATTTAAGGT GGTATTTGGC	60
AATGTGTCAG GCATCGTGGC AGTGTGCGTC AACTTCACCA GTTACGTCCA ACATGTCAAG	120
GAATTTACCC AACGTTCCTT GGTAGTTGAC CATGTGCGGC TGCTCCATTT CATGACGCCC	180

240

GAGACCATGA GGTGGGCAAC TGTTTTAGCC TGTCTTTTTA CCATTCTGTT GGCAATTTGA

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1799 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CCTGAATTGA G	ATGAAATGG	GGTCTATGCA	AAGCCTTTTT	GACAAAATTG	GCCAACTTTT	60
TGTGGATGCT T	TCACGGAGT	TCTTGGTGTC	CATTGTTGAT	ATCATTATAT	TTTTGGCCAT	120
TTTGTTTGGC T	TCACCATCG	CAGGTTGGCT	GGTGGTCTTT	TGCATCAGAT	TGGTTTGCTC	180
CGCGATACTC CO	GTGCGCGCC	CTGCCATTCA	CTCTGAGCAA	TTACAGAAGA	TCCTATGAGG	240
CCTTTCTCTC TO	CAGTGCCAG	GTGGACATTC	CCACCTGGGG	AACTAAACAT	CCTTTGGGGA	300
TGCTTTGGCA CO	CATAAGGTG	TCAACCCTGA	TTGATGAAAT	GGTGTCGCGT	CGAATGTACC	360
GCATCATGGA A	AAAGCAGGA	CAGGCTGCCT	GGAAACAGGT	AGTGAGCGAG	GCTACGCTGT	420
CTCGCATTAG TA	AGTTTGGAT	GTGGTGGCTC	ATTTTCAGCA	TCTTGCCGCC	ATTGAAGCCG	480
AGACCTGTAA A	TATCTGGCC	TCTCGGCTGC	CCATGCTACA	CCACCTGCGC	ATGACAGGGT	540
CAAATGTAAC CA	ATAGTGTAT	AATAGTACTT	TGAATCAGGT	GTTTGCTGTT	TTCCCAACCC	600
CTGGTTCCCG GC	CCAAAGCTT	CATGATTTCC	AGCAATGGCT	AATAGCTGTA	CATTCCTCTA	660

TATTTTCCTC	TGTTGCAGCT	TCTTGTACTC	TTTTTGTTGT	GCTGTGGTTG	CGGGTTCCAA	720
TGCTACGTAC	TGTTTTTGGT	TTCCGCTGGT	TAGGGGCAAT	TTTTCTTTCG	AACTCACGGT	780
GAATTACACG	GTGTGCCCGC	CTTGCCTCAC	CCGGCAAGCA	GCCGCAGAGG	CCTACGAACC	840
CGGCAGGTCC	CTTTGGTGCA	GGATAGGGCA	TGATCGATGT	GGGGAGGACG	ATCATGATGA	900
ACTAGGGTTT	GTGGTGCCGT	CTGGCCTCTC	CAGCGAAGGC	CACTTGACCA	GTGCTTACGC	960
CTGGTTGGCG	TCCCTGTCCT	TCAGCTATAC	GGCCCAGTTC	CATCCCGAGA	TATTCGGGAT	1020
AGGGAATGTG	AGTCGAGTCT	ATGTTGACAT	CAAGCACCAA	TTCATTTGCG	CTGTTCATGA	1080
TGGGCAGAAC	ACCACCTTGC	CCCACCATGA	CAACATTTCA	GCCGTGCTTC	AGACCTATTA	1140
CCAGCATCAG	GTCGACGGGG	GCAATTGGTT	TCACCTAGAA	TGGGTGCGTC	CCTTCTTTTC	1200
CTCTTGGTTG	GTTTTAAATG	TCTCTTGGTT	TCTCAGGCGT	TCGCCTGCAA	GCCATGTTTC	1260
AGTTCGAGTC	TTTCAGACAT	CAAGACCAAC	ACCACCGCAG	CGGCAGGCTT	TGCTGTCCTC	1320
CAAGACATCA	GTTGCCTTAG	GCATCGCAAC	TCGGCCTCTG	AGGCGATTCG	CAAAGTCCCT	1380
CAGTGCCGCA	CGGCGATAGG	GACACCCGTG	TATATCACTG	TCACAGCCAA	TGTTACCGAT	1440
GAGAATTATT	TGCATTCCTC	TGATCTTCTC	ATGCTTTCTT	CTTGCCTTTT	CTATGCTTCT	1500
GAGATGAGTG	AAAAGGGATT	TAAGGTGGTA	TTTGGCAATG	TGTCAGGCAT	CGTGGCAGTG	1560
TGCGTCAACT	TCACCAGTTA	CGTCCAACAT	GTCAAGGAAT	TTACCCAACG	TTCCTTGGTA	1620
GTTGACCATG	TGCGGCTGCT	CCATTTCATG	ACGCCCGAGA	CCATGAGGTG	GGCAACTGTT	1680
TTAGCCTGTC	TTTTTACCAT	TCTGTTGGCA	ATTTGAATGT	TTAAGTATGT	TGGGGAAATG	1740
CTTGACCGCG	GGCTGTTGCT	CGCAATTGCT	TTTTTTATGG	TGTATCGTGC	CGTCTTGTT	1799
(a) ==================================						

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 771 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATG Met 1	AAA Lys	TGG Trp	GGT Gly	CTA Leu 5	TGC Cys	AAA Lys	GCC Ala	TTT Phe	TTG Leu 10	ACA Thr	AAA Lys	TTG Leu	GCC Ala	AAC Asn 15	Phe		48
TTG Leu	TGG Trp	ATG Met	CTT Leu 20	TCA Ser	CGG Arg	AGT Ser	TCT Ser	TGG Trp 25	TGT Cys	CCA Pro	TTG Leu	TTG Leu	ATA Ile 30	Ser	TTA Leu		96
TAT Tyr	TTT Phe	TGG Trp 35	CCA Pro	TTT Phe	TGT Cys	TTG Leu	GCT Ala 40	TCA Ser	CCA Pro	TCG Ser	CAG Gln	GTT Val 45	Gly	TGG Trp	TGG Trp	=	L44
TCT Ser	TTT Phe 50	GCA Ala	TCA Ser	GAT Asp	TGG Trp	TTT Phe 55	GCT Ala	CCG Pro	CGA Arg	TAC Tyr	TCC Ser 60	Val	CGC Arg	GCC Ala	CTG Leu	. 1	L92
CCA Pro 65	TTC Phe	ACT Thr	CTG Leu	AGC Ser	AAT Asn 70	TAC Tyr	AGA Arg	AGA Arg	TCC Ser	TAT Tyr 75	GAG Glu	GCC Ala	TTT Phe	CTC Leu	TCT Ser 80		240
CAG Gln	TGC	CAG Gln	GTG Val	GAC Asp 85	ATT Ile	CCC Pro	ACC Thr	TGG Trp	GGA Gly 90	ACT Thr	AAA Lys	CAT His	CCT Pro	TTG Leu 95	Gly	2	888
ATG Met	CTT Leu	TGG Trp	CAC His 100	CAT His	AAG Lys	GTG Val	TCA Ser	ACC Thr 105	CTG Leu	ATT Ile	GAT Asp	GAA Glu	ATG Met 110	Val	TCG Ser	3	336
CGT Arg	CGA Arg	ATG Met 115	TAC Tyr	CGC Arg	ATC Ile	ATG Met	GAA Glu 120	AAA Lys	GCA Ala	GGA Gly	CAG Gln	GCT Ala 125	GCC Ala	TGG Trp	AAA Lys	3	884
CAG Gln	GTA Val 130	GTG Val	AGC Ser	GAG Glu	GCT Ala	ACG Thr 135	CTG Leu	TCT Ser	CGC Arg	ATT Ile	AGT Ser 140	AGT Ser	TTG Leu	GAT Asp	GTG Val	4	32
GTG Val 145	GCT Ala	CAT His	TTT Phe	CAG Gln	CAT His 150	CTT Leu	GCC Ala	GCC Ala	ATT Ile	GAA Glu 155	GCC Ala	GAG Glu	ACC Thr	TGT Cys	AAA Lys 160	4	80

														ACA (Thr 175		528
														TTT (Phe		576
													Phe	CAG Gln		624
TGG Trp	CTA Leu 210	ATA Ile	GCT Ala	GTA Val	CAT His	TCC Ser 215	TCT Ser	ATA Ile	TTT Phe	TCC Ser	TCT Ser 220	GTT Val	GCA Ala	GCT ' Ala	TCT Ser	672
											Pro			CGT Arg		720
														TCA Ser 255		768
TGA		•														771
(2)	INF	ORMA'	rion	FOR	SEQ	ID	NO : 6	7:								
		(i) s	SEQUI	ENCE	CHA	RACT	ERIS	TICS	:							

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Lys Trp Gly Leu Cys Lys Ala Phe Leu Thr Lys Leu Ala Asn Phe 1 5 10 15

Leu Trp Met Leu Ser Arg Ser Ser Trp Cys Pro Leu Leu Ile Ser Leu 20 25 30

Tyr Phe Trp Pro Phe Cys Leu Ala Ser Pro Ser Gln Val Gly Trp Trp 35 40 45

Ser Phe Ala Ser Asp Trp Phe Ala Pro Arg Tyr Ser Val Arg Ala Leu 50 55 60

Pro Phe Thr Leu Ser Asn Tyr Arg Arg Ser Tyr Glu Ala Phe Leu Ser 65 70 75 80

Gln Cys Gln Val Asp Ile Pro Thr Trp Gly Thr Lys His Pro Leu Gly
85 90 95

Met Leu Trp His His Lys Val Ser Thr Leu Ile Asp Glu Met Val Ser 100 105 110

Arg Arg Met Tyr Arg Ile Met Glu Lys Ala Gly Gln Ala Ala Trp Lys 115 120 125

Gln Val Val Ser Glu Ala Thr Leu Ser Arg Ile Ser Ser Leu Asp Val 130 135 140

Val Ala His Phe Gln His Leu Ala Ala Ile Glu Ala Glu Thr Cys Lys 145 150 155 160

Tyr Leu Ala Ser Arg Leu Pro Met Leu His His Leu Arg Met Thr Gly
165 170 175

Ser Asn Val Thr Ile Val Tyr Asn Ser Thr Leu Asn Gln Val Phe Ala 180 185 190

Val Phe Pro Thr Pro Gly Ser Arg Pro Lys Leu His Asp Phe Gln Gln
195 200 205

Trp Leu Ile Ala Val His Ser Ser Ile Phe Ser Ser Val Ala Ala Ser 210 215 220

Cys Thr Leu Phe Val Val Leu Trp Leu Arg Val Pro Met Leu Arg Thr 225 230 235 240

Val Phe Gly Phe Arg Trp Leu Gly Ala Ile Phe Leu Ser Asn Ser Arg 245 250 255

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 1..762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATG Met 1	GCT Ala	AAT Asn	AGC Ser	TGT Cys 5	ACA Thr	TTC Phe	CTC Leu	TAT Tyr	ATT Ile 10	TTC Phe	CTC Leu	TGT Cys	TGC Cys	AGC Ser 15	Phe	48
TTG Leu	TAC Tyr	TCT Ser	TTT Phe 20	TGT Cys	TGT Cys	GCT Ala	GTG Val	GTT Val 25	GCG Ala	GGT Gly	TCC Ser	AAT Asn	GCT Ala 30	Thr	TAC Tyr	96
TGT Cys	TTT Phe	TGG Trp 35	TTT Phe	CCG Pro	CTG Leu	GTT Val	AGG Arg 40	GGC Gly	AAT Asn	TTT Phe	TCT Ser	TTC Phe 45	Glu	CTC Leu	ACG Thr	144
GTG Val	AAT Asn 50	TAC Tyr	ACG Thr	GTG Val	TGC Cys	CCG Pro 55	CCT Pro	TGC Cys	CTC Leu	ACC Thr	CGG Arg 60	Gln	GCA Ala	GCC Ala	GCA Ala	192
GAG Glu 65	GCC Ala	TAC Tyr	GAA Glu	CCC Pro	GGC Gly 70	AGG Arg	TCC Ser	CTT Leu	TGG Trp	TGC Cys 75	AGG Arg	ATA Ile	GGG Gly	CAT His	GAT Asp 80	240
CGA Arg	TGT Cys	GGG Gly	GAG Glu	GAC Asp 85	GAT Asp	CAT His	GAT Asp	GAA Glu	CTA Leu 90	GGG Gly	TTT Phe	GTG Val	GTG Val	CCG Pro 95	Ser	288
GGC Gly	CTC Leu	TCC Ser	AGC Ser 100	GAA Glu	GGC Gly	CAC His	TTG Leu	ACC Thr 105	Ser	GCT Ala	TAC Tyr	GCC Ala	TGG Trp 110	Leu	GCG Ala	336
TCC Ser	CTG Leu	TCC Ser 115	TTC Phe	AGC Ser	TAT Tyr	ACG Thr	GCC Ala 120	CAG Gln	TTC Phe	CAT [.] His	CCC Pro	GAG Glu 125	ATA Ile	TTC Phe	GGG Gly	384
ATA Ile	GGG Gly 130	AAT Asn	GTG Val	AGT Ser	CGA Arg	GTC Val 135	Tyr	GTT Val	GAC Asp	ATC Ile	AAG Lys 140	CAC His	CAA Gln	TTC Phe	ATT Ile	432
TGC Cys 145	GCT Ala	GTT Val	CAT His	GAT Asp	GGG Gly 150	CAG Gln	AAC Asn	ACC Thr	ACC Thr	TTG Leu 155	CCC Pro	CAC His	CAT His	GAC Asp	AAC Asn 160	480
ATT Ile	TCA Ser	GCC Ala	GTG Val	CTT Leu 165	CAG Gln	ACC Thr	TAT Tyr	TAC Tyr	CAG Gln 170	CAT His	CAG Gln	GTC Val	GAC Asp	GGG Gly 175	GGC Gly	528
AAT Asn	TGG Trp	TTT Phe	CAC His 180	CTA Leu	GAA Glu	TGG Trp	GTG Val	CGT Arg 185	CCC Pro	TTC Phe	TTT Phe	TCC Ser	TCT Ser 190	Trp	TTG Leu	576

Val	Leu	Asn 195	Val	TCT Ser	TGG Trp	TTT Phe	CTC Leu 200	Arg	CGT Arg	TCG Ser	CCT Pro	GCA Ala 205	Ser	CAT His	GTT Val
TCA Ser	GTT Val 210	CGA Arg	GTC Val	TTT Phe	CAG Gln	ACA Thr 215	TCA Ser	AGA Arg	CCA Pro	ACA Thr	CCA Pro 220	CCG Pro	CAG Gln	CGG Arg	CAG Gln
GCT Ala 225	TTG Leu	CTG Leu	TCC Ser	TCC Ser	AAG Lys 230	ACA Thr	TCA Ser	GTT Val	GCC Ala	TTA Leu 235	GGC Gly	ATC Ile	GCA Ala	ACT Thr	CGG Arg 240
CCT Pro TAG	CTG Leu	AGG Arg	CGA Arg	TTC Phe 245	GCA Ala	AAG Lys	TCC Ser	CTC Leu	AGT Ser 250	GCC Ala	GCA Ala	CGG Arg	CGA Arg		
(2)				FOR		•				-					
		(i) S		ENCE LE1						3					
			(B)	TY	?E: a	amino		id		_					
			(D)	LOI	CHO	3 L	r +11C	スエ							
•	į)	Li) N		CULE											
			OLE		TYPI	E: pı	cote	in	Q ID	NO:	59:			-	
Met 1	()	ci) S	MOLE (CULE	TYPE	E: pi	cote: TION	in : SE(Cys	Cys	Ser 15	Phe
1	() Ala	ci) S Asn	MOLE(SEQUI Ser	CULE ENCE Cys	TYPE DESC Thr	E: pi CRIPT Phe	cote: CION Leu	in : SE(Tyr	Ile 10	Phe	Leu			15	
Leu	(x Ala Tyr	ci) S Asn Ser	MOLE SEQUE Ser Phe 20	CULE ENCE Cys 5	TYPE DESC Thr	E: pr CRIPT Phe Ala	rote: FION Leu Val	in : SE(Tyr Val 25	Ile 10 Ala	Phe Gly	Leu Ser	Asn	Ala 30	15 Thr	Tyr
Leu Cys	() Ala Tyr Phe	Asn Ser Trp 35	MOLEG SEQUE Ser Phe 20 Phe	CULE ENCE Cys 5 Cys	TYPE DESC Thr Cys	E: process pro	rote: FION Leu Val Arg 40	Tyr Val 25	Ile 10 Ala Asn	Phe Gly Phe	Leu Ser Ser	Asn Phe 45	Ala 30 Glu	15 Thr Leu	Tyr Thr
Leu Cys Val	Ala Tyr Phe Asn 50	Asn Ser Trp 35	MOLEG SEQUE Ser Phe 20 Phe Thr	CULE ENCE Cys 5 Cys Pro	TYPE DESC Thr Cys Leu Cys	E: pro	rote: FION Leu Val Arg 40 Pro	in ESE Tyr Val 25 Gly Cys	Ile 10 Ala Asn Leu	Phe Gly Phe Thr	Leu Ser Ser Arg	Asn Phe 45 Gln	Ala 30 Glu Ala	15 Thr Leu Ala	Tyr Thr Ala
Leu Cys Val Glu 65	Ala Tyr Phe Asn 50 Ala	Asn Ser Trp 35 Tyr Tyr	MOLEO SEQUE Ser Phe 20 Phe Thr	CULE ENCE Cys 5 Cys Pro Val	TYPE DESC Thr Cys Leu Cys Gly 70	Phe Ala Val Pro 55 Arg	Cote: FION Leu Val Arg 40 Pro	in E SEG Tyr Val 25 Gly Cys Leu	Ile 10 Ala Asn Leu Trp	Phe Gly Phe Thr Cys 75	Leu Ser Ser Arg 60	Asn Phe 45 Gln Ile	Ala 30 Glu Ala Gly	15 Thr Leu Ala His	Tyr Thr Ala Asp 80

Ser Leu Ser Phe Ser Tyr Thr Ala Gln Phe His Pro Glu Ile Phe Gly 115 120 125

Ile Gly Asn Val Ser Arg Val Tyr Val Asp Ile Lys His Gln Phe Ile 130 135 140

Cys Ala Val His Asp Gly Gln Asn Thr Thr Leu Pro His His Asp Asn 145 150 155 160

Ile Ser Ala Val Leu Gln Thr Tyr Tyr Gln His Gln Val Asp Gly Gly 165 170 175

Asn Trp Phe His Leu Glu Trp Val Arg Pro Phe Phe Ser Ser Trp Leu 180 185 190

Val Leu Asn Val Ser Trp Phe Leu Arg Arg Ser Pro Ala Ser His Val 195 200 205

Ser Val Arg Val Phe Gln Thr Ser Arg Pro Thr Pro Pro Gln Arg Gln 210 215 220

Ala Leu Leu Ser Ser Lys Thr Ser Val Ala Leu Gly Ile Ala Thr Arg 225 230 235 240

Pro Leu Arg Arg Phe Ala Lys Ser Leu Ser Ala Ala Arg Arg 245 250

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

48	CTC TTG Leu Leu 15	AAA TGT Lys Cys	TTT Phe	Gly	GTT Val 10	TTG Leu	CTC Leu	TTC Phe	Leu	CTT Leu 5	TCC Ser	GCG Ala	Gly	ATG Met 1
96	CTT TCA Leu Ser	TCG AGT Ser Ser 30	AGT Ser	TTC Phe	Cys	CCA Pro 25	AAG Lys	TGC Cys	GCC Ala	TTC Phe	GCG Ala 20	CAG Gln	TCT Ser	GTT Val
144	CTC CAA Leu Gln	GCT GTC Ala Val 45	TTT Phe	GGC Gly	GCA Ala	Ala	GCA Ala 40	ACC Thr	ACC Thr	AAC Asn	ACC Thr	AAG Lys 35	ATC Ile	GAC Asp
192	ATT CGC lle Arg		TCT Ser	GCC Ala	TCG Ser	AAC Asn	CGC Arg	CAT His 55	AGG Arg	CTT Leu	TGC Cys	AGT Ser	ATC Ile 50	GAC Asp
240	ATC ACT Ile Thr 80	GTG TAT Val Tyr	Pro	ACA Thr 75	GGG Gly	ATA Ile	GCG Ala	Thr	CGC Arg 70	TGC Cys	CAG Gln	CCT Pro	GTC Val	AAA Lys 65
288	GAT CTT Asp Leu 95	TCC TCT Ser Ser	CAT His	Leu	TAT Tyr 90	AAT Asn	GAG Glu	GAT Asp	ACC Thr	GTT Val 85	AAT Asn	GCC Ala	ACA Thr	GTC Val
336	GAA AAG Glu Lys	ATG AGT Met Ser 110	GAG Glu	TCT Ser	GCT Ala	TAT Tyr 105	TTC Phe	CTT Leu	TGC Cys	TCT Ser	TCT Ser 100	CTT Leu	ATG Met	CTC Leu
384	GTG TGC Val Cys	GTG GCA Val Ala 125												
432	CAA CGT Gln Arg	TTT ACC Phe Thr	GAA Glu 140	AAG Lys	GTC Val	CAT His	CAA Gln	GTC Val 135	TAC Tyr	AGT Ser	ACC Thr	TTC Phe	AAC Asn 130	GTC Val
480	CCC GAG Pro Glu 160	ATG ACG Met Thr	TTC Phe	CAT His 155	CTC Leu	CTG Leu	CGG Arg	GTG Val	CAT His 150	GAC Asp	GTT Val	GTA Val	TTG Leu	TCC Ser 145
528	CTG TTG Leu Leu 175	ACC ATT Thr Ile	TTT Phe	CTT Leu	TGT Cys 170	GCC Ala	TTA Leu	GTT Val	ACT Thr	GCA Ala 165	TGG Trp	AGG Arg	ATG Met	ACC Thr
537						•					· · .	TGA		GCA Ala

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Gly Ala Ser Leu Leu Phe Leu Leu Val Gly Phe Lys Cys Leu Leu 1 5 10 15

Val Ser Gln Ala Phe Ala Cys Lys Pro Cys Phe Ser Ser Ser Leu Ser 20 25 30

Asp Ile Lys Thr Asn Thr Thr Ala Ala Ala Gly Phe Ala Val Leu Gln 35 40 45

Asp Ile Ser Cys Leu Arg His Arg Asn Ser Ala Ser Glu Ala Ile Arg 50 55 60

Lys Val Pro Gln Cys Arg Thr Ala Ile Gly Thr Pro Val Tyr Ile Thr 65 70 75 80

Val Thr Ala Asn Val Thr Asp Glu Asn Tyr Leu His Ser Ser Asp Leu
85 90 95

Leu Met Leu Ser Ser Cys Leu Phe Tyr Ala Ser Glu Met Ser Glu Lys
100 105 110

Gly Phe Lys Val Val Phe Gly Asn Val Ser Gly Ile Val Ala Val Cys 115 120 125

Val Asn Phe Thr Ser Tyr Val Gln His Val Lys Glu Phe Thr Gln Arg 130 135 140

Ser Leu Val Val Asp His Val Arg Leu Leu His Phe Met Thr Pro Glu
145 150 155 160

Thr Met Arg Trp Ala Thr Val Leu Ala Cys Leu Phe Thr Ile Leu Leu 165 170 175

Ala Ile

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome
 - (C) INDIVIDUAL ISOLATE: Lelystad
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..747
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

48		AGC TGT TCG Ser Cys Ser								
96	e Ser Leu	TTG CCA TTT Leu Pro Phe 30								
144		TAC TGG TCT Tyr Trp Ser 45			Gln					
192		GCT CTG CCA Ala Leu Pro 60								
240		TTG CCC AAC Leu Pro Asn								
288		TTG GGT ATG Leu Gly Met	Pro							
336	g Arg Ile	GTC TCT CGT Val Ser Arg 110		Glu						
384		TGG AAG CAG Trp Lys Gln 125			Gln					
432		GAT ATA GTT Asp Ile Val 140				Leu			Ala	

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Gln Trp Gly His Cys Gly Val Lys Ser Ala Ser Cys Ser Trp Thr 1 5 10 15

Pro Ser Leu Ser Ser Leu Leu Val Trp Leu Ile Leu Pro Phe Ser Leu 20 25 30

Pro Tyr Cys Leu Gly Ser Pro Ser Gln Asp Gly Tyr Trp Ser Phe Phe 35 40 45

Ser Glu Trp Phe Ala Pro Arg Phe Ser Val Arg Ala Leu Pro Phe Thr 50 55 60

Leu Pro Asn Tyr Arg Arg Ser Tyr Glu Gly Leu Leu Pro Asn Cys Arg 65 70 75 80

Pro Asp Val Pro Gln Phe Ala Val Lys His Pro Leu Gly Met Phe Trp 85 90 95

His Met Arg Val Ser His Leu Ile Asp Glu Met Val Ser Arg Arg Ile 100 105 110

Tyr Gln Thr Met Glu His Ser Gly Gln Ala Ala Trp Lys Gln Val Val 115 120 125

Gly Glu Ala Thr Leu Thr Lys Leu Ser Gly Leu Asp Ile Val Thr His 130 135 140

Phe Gln His Leu Ala Ala Val Glu Ala Asp Ser Cys Arg Phe Leu Ser 145 150 155 160

Ser Arg Leu Val Met Leu Lys Asn Leu Ala Val Gly Asn Val Ser Leu 165 170 175

Gln Tyr Asn Thr Thr Leu Asp Arg Val Glu Leu Ile Phe Pro Thr Pro 180 185 190

Gly Thr Arg Pro Lys Leu Thr Asp Phe Arg Gln Trp Leu Ile Ser Val 195 200 205

His Ala Ser Ile Phe Ser Ser Val Ala Ser Ser Val Thr Leu Phe Ile 210 215 220

Val Leu Trp Leu Arg Ile Pro Ala Leu Arg Tyr Val Phe Gly Phe His 225 230 235 240

Trp Pro Thr Ala Thr His His Ser Ser 245

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 798 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

						_								
48	TTC ATC y Phe Ile 15	TGT GGC Cys Gly	CTC Leu	Phe	TTT Phe 10	CAT His	TTC Phe	CGC Arg	GCA Ala	TGT Cys 5	CAG Gln	CAT His	GCT Ala	ATG Met 1
96	T ACG CTA r Thr Leu 0	AGC TCT Ser Ser 30	TCC Ser	AAT Asn	Ser	GCT Ala 25	TTG Leu	GCT Ala	AGT Ser	CAT	GTT Val 20	CTT Leu	TAC Tyr	TGT Cys
144	CTG ACC u Leu Thr	TTC GAG Phe Glu 45	TCA Ser	ACA Thr	AAC Asn	GGC Gly	CAC His 40	GCC Ala	TTG Leu	CCA Pro	TTT Phe	TGG Trp 35	TTT Phe	TGT Cys
192	GCT CGC a Ala Arg	CAA GCG Gln Ala	AGT Ser 60	ACC Thr	TCT Ser	TGT Cys	Pro	ATG Met 55	TGC Cys	ATA Ile	ACC Thr	TAC Tyr	AAC Asn 50	ATC Ile
240	CAT GAC y His Asp 80	ATA GGG Ile Gly	AAA Lys	TGC Cys 75	TGG Trp	ATG Met	AAC Asn	CGT Arg	GGT Gly 70	CCC Pro	GAG Glu	CTC Leu	AGG Arg	CAA Gln 65
288	CCG TCC e Pro Ser 95	TCC ATC Ser Ile	ATG Met	TTA Leu	TTG Leu 90	GAG Glu	GAT Asp	CAT His	GAC Asp	CGT Arg 85	GAG Glu	GAG Glu	TGT Cys	AGG Arg
336	GCT TTT u Ala Phe 0	TGG CTG Trp Leu 110	GCT Ala	TAT Tyr	TAT Tyr	GGT Gly 105	GAG Glu	CTT Leu	AAA Lys	CTC Leu	AAC Asn 100	GAC Asp	TAC Tyr	GGG Gly
384	GGG ATA e Gly Ile	TTG TTC Leu Phe 125	GAG Glu	CCG Pro	CAT His	TTC Phe	CAA Gln 120	GCC Ala	GCG Ala	TAC Tyr	TCC Ser	TTT Phe 115	TCC Ser	TTG Leu
432	ATT TGT e Ile Cys	CAG TTC . Gln Phe	CAC His 140	CGA Arg	AAG _. Lys	GAC Asp	GTG Val	TTC Phe 135	GTC Val	CGC Arg	TCG Ser	GTG Val	AAT Asn 130	GGG Gly
480	AAC ATC S Asn Ile 160	GGA CAC	ACC (TCT Ser 155	GTA Val	ACC Thr	TCA Ser	AAT Asn	CAC His 150	GGA Gly	GAT Asp	CAT His	GAG Glu	GCC Ala 145
528	GGC AAT Gly Asn 175	GAC GGG (Asp. Gly	ATA (CAA Z Gln	CAC His 170	CAC His	TAC Tyr	TAT Tyr	GCA Ala	GCG Ala 165	TAT Tyr	TTA Leu	GCA Ala	TCC Ser

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0

TGG Trp	TTC Phe	CAT His	TTG Leu 180	GAA Glu	TGG Trp	CTG Leu	CGG Arg	CCA Pro 185	Leu	TTT Phe	TCT Ser	TCC Ser	TGG Trp 190	CTG Leu	GTG Val	.	57
CTC Leu	AAC Asn	ATA Ile 195	TCA Ser	TGG Trp	TTT Phe	CTG Leu	AGG Arg 200	CGT Arg	TCG Ser	CCT Pro	GTA Val	AGC Ser 205	CCT Pro	GTT Val	TCT Ser	ϵ	52
CGA Arg	CGC Arg 210	ATC Ile	TAT Tyr	CAG Gln	ATA Ile	TTG Leu 215	AGA Arg	CCA Pro	ACA Thr	CGA Arg	CCG Pro 220	CGG Arg	CTG . Leu	CCG Pro	GTT Val	6	57
TCA Ser 225	TGG Trp	TCC Ser	TTC Phe	AGG Arg	ACA Thr 230	TCA Ser	ATT Ile	GTT Val	TCC Ser	GAC Asp 235	CTC Leu	ACG Thr	GGG Gly	TCT Ser	CAG Gln 240	7	72
CAG Gln	CGC Arg	AAG Lys	AGA Arg	AAA Lys 245	TTT Phe	CCT Pro	TCG Ser	GAA Glu	AGT Ser 250	CGT Arg	CCC Pro	AAT Asn	GTC Val	GTG Val 255	AAG Lys	7	76
	TCG Ser								TAA		٠.					7	79
(2)	INFO	RMAG	CION	FOR	SEQ	ID 1	NO: 75	ō:	`								
		(i) S	(A) (B)	ĻE1 TYI	NGTH:	: 265 amino	ERIS' am: ac: linea	ino a id		S							•
	(i	i) M	OLEC	CULE	TYPE	E: pi	cote	in									
	(x	ci) S	EQUE	ENCE	DESC	CRIPT	CION	: SE	Q ID	NO:	75:	•					
Met	Δla	His	Gln	Cve	ΔΊΞ	Δνα	Dha	ціс	Dhe	Dho	LON	Cara	C1.,,	Dho	T1.		

Met Ala His Gln Cys Ala Arg Phe His Phe Phe Leu Cys Gly Phe
1 5 10 15

Cys Tyr Leu Val His Ser Ala Leu Ala Ser Asn Ser Ser Ser Thr Leu 20 25 30

Cys Phe Trp Phe Pro Leu Ala His Gly Asn Thr Ser Phe Glu Leu Thr 35 40 45

Ile Asn Tyr Thr Ile Cys Met Pro Cys Ser Thr Ser Gln Ala Ala Arg 50 55 60

Gln Arg Leu Glu Pro Gly Arg Asn Met Trp Cys Lys Ile Gly His Asp 65 70 75 80 Arg Cys Glu Glu Arg Asp His Asp Glu Leu Leu Met Ser Ile Pro Ser 85 90 95

Gly Tyr Asp Asn Leu Lys Leu Glu Gly Tyr Tyr Ala Trp Leu Ala Phe 100 105 110

Leu Ser Phe Ser Tyr Ala Ala Gln Phe His Pro Glu Leu Phe Gly Ile 115 120 125

Gly Asn Val Ser Arg Val Phe Val Asp Lys Arg His Gln Phe Ile Cys 130 135 140

Ala Glu His Asp Gly His Asn Ser Thr Val Ser Thr Gly His Asn Ile 145 150 155 160

Ser Ala Leu Tyr Ala Ala Tyr Tyr His His Gln Ile Asp Gly Gly Asn 165 170 175

Trp Phe His Leu Glu Trp Leu Arg Pro Leu Phe Ser Ser Trp Leu Val 180 185 190

Leu Asn Ile Ser Trp Phe Leu Arg Arg Ser Pro Val Ser Pro Val Ser 195 200 205

Arg Arg Ile Tyr Gln Ile Leu Arg Pro Thr Arg Pro Arg Leu Pro Val 210 215 220

Ser Trp Ser Phe Arg Thr Ser Ile Val Ser Asp Leu Thr Gly Ser Gln 225 230 235 240

Gln Arg Lys Arg Lys Phe Pro Ser Glu Ser Arg Pro Asn Val Lys 245 250 255

Pro Ser Val Leu Pro Ser Thr Ser Arg
260 265

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Lelystad
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG Met 1	GCT Ala	GCG Ala	GCC Ala	ACT Thr 5	CTT Leu	TTC Phe	TTC Phe	CTG Leu	GCT Ala 10	Gly	GCT Ala	CAA Gln	CAT His	ATC Ile 15	Met	48	
													CAT His 30	Leu	TCA Ser	96	
															CAG Gln	144	
													CAA Gln		AAA Lys	192	
ATT Ile 65	TCC Ser	TTC Phe	GGA Gly	AAG Lys	TCG Ser 70	TCC Ser	CAA Gln	TGT .Cys	CGT Arg	GAA Glu 75	Ala	GTC Val	GGT .Gly	ACT Thr	CCC Pro 80	240	
										Asp					TAC Tyr	288	
													GCC Ala 110		GAA Glu	336	
								Ile							GTT Val	384	
Val	Ser 130	Ala	Cys	Val	Asn	Phe 135	Thr	Asp	Tyr	Val	Ala 140	His		Thr	Gln	432	
His 145	Thr	Gln	Gln	His	His 150	Leu	Val	Ile	Asp	His 155	Ile	Arg	TTG Leu	Leu	His 160	480	-
Phe	Leu	Thr	Pro	Ser 165	Ala	Met	Arg						GCT Ala		Leu	528	
			CTC Leu 180				TGA						ru na na			552	

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:
- Met Ala Ala Ala Thr Leu Phe Phe Leu Ala Gly Ala Gln His Ile Met
 1 5 10 15
- Val Ser Glu Ala Phe Ala Cys Lys Pro Cys Phe Ser Thr His Leu Ser 20 25 30
- Asp Ile Glu Thr Asn Thr Thr Ala Ala Ala Gly Phe Met Val Leu Gln
 35 40 45
- Asp Ile Asn Cys Phe Arg Pro His Gly Val Ser Ala Ala Gln Glu Lys
 50 55 60
- Ile Ser Phe Gly Lys Ser Ser Gln Cys Arg Glu Ala Val Gly Thr Pro 65 70 75 80
- Gln Tyr Ile Thr Ile Thr Ala Asn Val Thr Asp Glu Ser Tyr Leu Tyr 85 90 95
- Asn Ala Asp Leu Leu Met Leu Ser Ala Cys Leu Phe Tyr Ala Ser Glu 100 105 110
- Met Ser Glu Lys Gly Phe Lys Val Ile Phe Gly Asn Val Ser Gly Val
- Val Ser Ala Cys Val Asn Phe Thr Asp Tyr Val Ala His Val Thr Gln 130 135 140
- His Thr Gln Gln His His Leu Val Ile Asp His Ile Arg Leu Leu His 145 150 155 160
- Phe Leu Thr Pro Ser Ala Met Arg Trp Ala Thr Thr Ile Ala Cys Leu 165 170 175

Phe Ala Ile Leu Leu Ala Ile 180